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| (57) Abstract | | | |
| <p>Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.</p> | | | |

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NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS

FIELD OF THE INVENTION

5 The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

BACKGROUND OF THE INVENTION

10 Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a
15 tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

20 Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases
25 can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

- 5 Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 10 Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

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Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon tissue.

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of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393.

Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503.

Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

- 5 Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

- 10 Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 15 Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 43 shows the sequence for the mRNA encoding CBC1. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 20 Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

- 25 Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

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DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzi et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al, *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 91986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

5 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA
10 and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both
15 double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine,
20 cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

25 A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

30 The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or dysregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

- 5 A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

- 10 As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare
15 the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms
20 (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

- 25 In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the
30 sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); <http://blast.wustl.edu/blast/REACRCE.html>]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures.

A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al.,

both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can

include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

| | | Chart I |
|----|------------------|-------------------------|
| | | Exemplary Substitutions |
| 5 | Original Residue | |
| | Ala | Ser |
| | Arg | Lys |
| | Asn | Gln, His |
| | Asp | Glu |
| 10 | Cys | Ser |
| | Gln | Asn |
| | Glu | Asp |
| | Gly | Pro |
| | His | Asn, Gln |
| 15 | Ile | Leu, Val |
| | Leu | Ile, Val |
| | Lys | Arg, Gln, Glu |
| | Met | Leu, Ile |
| | Phe | Met, Leu, Tyr |
| 20 | Ser | Thr |
| | Thr | Ser |
| | Trp | Tyr |
| | Tyr | Trp, Phe |
| | Val | Ile, Leu |

25 Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the

30 greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is

35 substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or

40 removed.

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Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAAQ9p4, CAA9p4MAPS, CAA89p5 and CAA9p5MAPS.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975).

In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol.,

222-581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcun, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radiolabels to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^{-4} - 10^{-6} M $^{-1}$, with a preferred range being 10^{-7} - 10^{-9} M $^{-1}$.

In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with
5 nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a
10 preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients
15 allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting
20 with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the CRC protein find use in *in situ* imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is
25 detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological
30 imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

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chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreuleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

5 In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

10 In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification
15 such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target
20 sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin.
25 For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S.
30 Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt
10 concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

15 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise
20 improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

25 The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression
30 profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes
5 whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular
10 state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent.
15 After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in
20 normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral
30 construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein.
In one embodiment the CRC protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CRC proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound

5 material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in

10 screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding

15 determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as

20 magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for

25 detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins,

30 for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to
5 either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally
10 labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that
15 otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as
20 above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein.
25 The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in
30 colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

CAA2, CAA9, CGA7 and/or CGA8*, preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

5 In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

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ways, orally, parenterally e.g., subcutaneously, intrapentoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

5 The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying
10 agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes
15 comprising determining all or part of the sequence of at least one endogeneous CRC genes in a cell. As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include
20 comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the
25 sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

In another preferred embodiment CRC genes are used as probed to determine the chromosomal
30 localization of the CRC genes. Information such as chromosomal localization finds use in providing a

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogenous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogenous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the endogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogenous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

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A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

5 The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

10 The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or
15 otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable
20 base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines
25 and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

30 Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

- 5 In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, *Nature Biotechnology*, 16:1304-1305 (1998).

- 10 In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of
15 CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

- In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to
20 the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.

- In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene
25 will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.

- 30 It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

- 5 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

Example 1

1.0 Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

- Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.
- 1.5

HOMOGENIZATION

- Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.
- 2.0

- Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.
- 2.5

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.
Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.
Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

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Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

- 5 Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

- 10 Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.
- 15

Purify poly A⁺ mRNA from total RNA or clean up total RNA with Qiagen's

- 20 RNeasy kit

Purification of poly A⁺ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.

25

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A⁺ mRNA has occurred.

- 30 Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated.

Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

10 Ethanol Precipitation

Add 0.4 vol. of 7.5 M NH_4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood.

15 (Do not speed vacuum). Suspend pellet in DEPC H_2O at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

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Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of
 5 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

Add: 91ul DEPC H2O

1.0 30ul 5X 2nd Strand Buffer
 3ul 10mM dNTP mix
 1ul 10U/ul *E. coli* DNA Ligase
 4ul 10U/ul *E. coli* DNA Polymerase
 1ul 2U/ul RNase H

1.5 Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C.
 Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:

2.0 Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH4OAc and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove
 2.5 as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

3.0 Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)
 2ul T7 10xGTP (75mM) (Ambion)
 1.5ul T7 10xCTP (75mM) (Ambion)

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- 1.5ul T7 10xUTP (75mM) (Ambion)
 3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or
 Enzo)
 3.75ul 10mM Bio-16-CTP (Enzo)
 5 2ul 10x T7 transcription buffer (Ambion)
 2ul 10x T7 enzyme mix (Ambion)

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

- 10 cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

- 15 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer.
 Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

- 200 mM Tris-acetate, pH 8.1
 500 mM KOAc
 20 150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

- 25 200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

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Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

50 pM 948-b control oligo

1.5 pM BioB

5 pM BioC

5 25 pM BioD

100 pM CRE

0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA

to 300 ul with 1xMES hyb. buffer

10 The instruction manuals for the products used herein are incorporated herein in their entirety.

Labeling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

(see example 1 for steps from tissue to IVT)

15 IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl

H₂O: µl

14 µl

20 - Incubate 70°C, 10 min. Put on ice.

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

25 H₂O: 2.4 µl

Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

16 µl

30 - Add to hybridization reaction.

- Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 μ l each of 100mM dATP, dCTP, and dGTP; 10 μ l of 100mM dTTP to 15 μ l H₂O. dNTPs from Pharmacia)

| | | |
|---|---|------------------------|
| 5 | | 86 µl H ₂ O |
| | - Add 1.5 µl 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min. | 10 µl 10N NaOH |
| | | 4 µl 50mM EDTA |

500 μ l TE/sample spin at 7000g for 10 min, save flow through for purification

- Add 1 μ l of 1/100 dil of DNase/30 μ l Rx and incubate at 37°C for 15 min.

- Add:

Na pyro phosphate: 7.5 μ l

Put on slide and hybridize overnight at 64°C.

1X SSC: 5 min. 12.5 mls 20X SSC in 250mls H₂O

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0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropriate PMT's and channels.

The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors from a variety of stages of the disease. The genes that are up regulated in the tumors (overall) were also found to be expressed at a limited amount or not at all in the body map. The body map for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney, Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall) versus normal colon were not selected for their expression or lack of expression in the body map. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2 shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815 upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows 1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Example 2

Expression studies were performed herein.

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18 and 19 have a solubility of 1 mg/ 1 ml H₂O.

As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

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As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

CLAIMS

We claim:

1. A method of screening drug candidates comprising:
 - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
 - b) adding a drug candidate to said cell; and
 - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.
6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
 - a) administering said drug to a patient;
 - b) removing a cell sample from said patient; and
 - c) determining the expression profile of said cell.
7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.

9. A method of diagnosing colorectal cancer comprising:

a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and

b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;

wherein a difference in said expression indicates that the first individual has colorectal cancer.

10. An antibody which specifically binds to CJA8, or a fragment thereof.

11. An antibody which specifically binds to CAA9, or a fragment thereof.

12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.

14. The antibody of Claim 10, wherein said antibody is a humanized antibody.

15. The antibody of Claim 10, wherein said antibody is an antibody fragment.

16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:

a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof; and

b) determining the binding of said CCMP or fragment thereof and said antibody.

17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CAJ8 or a fragment thereof.

18. The method of Claim 17 wherein said cell is a cell of an individual.

19. The method of Claim 18 wherein said individual has cancer.

20. The method of Claim 17 wherein said antibody is a humanized antibody.
21. The method of Claim 17 wherein said antibody is an antibody fragment.
22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.
- 5 23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.
24. A composition comprising the peptide of Claim 23.
25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.
- 10 26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.
27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
- 15 28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.
- 20 30. The method of Claim 29 wherein said inhibitor is an antibody.
31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

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32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

5 33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.

34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.

35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.

10 36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.

37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.

38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

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FIGURE 1

| Primary Key | Fold upregulated in tumor over normal colon | Accession | Unigene CLUSTER | Unigene Descriptor |
|-------------|---|---------------|--------------------|--|
| 37677 | >10 | AA460530 | Hs 98394 | Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds |
| 6449 | >10 | X95986 | Hs 32936 | H sapiens mRNA for NRK apoptotic inducer protein |
| 4178 | >10 | U30246 | Hs 110736 | Human bimekade sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds |
| 18330 | >10 | AA218722 | Hs 54481 | Human mRNA for apolipoprotein E receptor 2 complete cds |
| 5692 | >10 | X17444 | Hs 2707 | G1 to S phase transition 1 |
| 16810 | >10 | AA053636 | Hs 129849 | PEK1 |
| 33109 | >10 | W59961 | Hs 27564 | Human mRNA for KIAA0389 gene complete cds |
| 37246 | >10 | AA449311 | Hs 98658 | Homo sapiens midline checkpoint protein kinase (BUB1) mRNA complete cds |
| 2867 | >10 | M68997 | Hs 2173 | Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific) |
| 14338 | >10 | AA598712 | Hs 23723 | ESTs Weakly similar to ORF YPL212c [S cerevisiae] |
| 4676 | 9.6 | U85208 | Hs 78619 | Homo sapiens human gamma-glutamyl hydrolase (IGH) mRNA complete cds |
| 2192 | 7.8 | L48211 | Hs 20954 | Homo Sapiens angiotensin II receptor gene complete cds |
| 5793 | 7.4 | X54542 | Hs 83758 | CDC28 protein kinase 2 |
| 18231 | 6.3 | AA199747 | Hs 79025 | Human mRNA for KIAA0096 gene partial cds |
| 6061 | 6.1 | X98314 | Hs 2704 | Gliothione peroxidase 2 gastrointestinal |
| 27117 | 5.0 | AA405098 | Hs 38178 | ESTs Weakly similar to MOESIN/ZIPK/PAK1 HOMOLOG [D.melanogaster] |
| 12659 | 5.0 | AA417030 | Hs 5101 | Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds |
| 1106 | 4.8 | HG2981-HT3127 | | EST - HG2981-HT3127 |
| 2157 | 4.6 | L41939 | Hs 89403 | Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds |
| 13193 | 4.4 | AA442763 | Hs 20483 | ESTs Highly similar to GZMITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus] |
| 5690 | 4.4 | X17620 | Hs 118638 | NUCLEOSIDE DIPHOSPHATE KINASE A |
| 28050 | 4.1 | AA475139 | Hs 75393 | Acid phosphatase 1 soluble |
| 4540 | 3.5 | U48807 | Hs 2359 | Human MAP kinase phosphatase (MKP-2) mRNA complete cds |
| 26105 | 3.1 | AA242133 | Hs 48915 | Homo sapiens serine/threonine kinase (BTA) mRNA complete cds |
| 19177 | 3.1 | H10894 | Hs 12338 | ESTs |
| 5780 | 3.1 | X54489 | Hs 789 | GRO1 oncogene (melanoma growth stimulating activity alpha) |
| 33620 | 3.0 | W83943 | Hs 59509 | ESTs |
| 4536 | 2.9 | U48705 | Hs 75562 | Receptor protein-tyrosine kinase EDDR1 |
| 5928 | 2.9 | X62048 | Hs 75188 | WEE1 LIKE PROTEIN KINASE |
| 28258 | 2.8 | AA505133 | Hs 62273 | ESTs |
| 21256 | 2.7 | R09795 | Hs 151385 | Homo sapiens mRNA for KIAA0864 protein partial cds |

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FIGURE 1 (CONT.)

| | | | | |
|-------|-----|----------|--------------|---|
| 27746 | 2.5 | AA453159 | Hs 41723 | Human kinase-like spindle protein HKSP (HKSP) mRNA complete cds |
| 25310 | 2.5 | AA046745 | Hs 110457 | ESTs |
| 2640 | 2.4 | M30448 | EST - M30448 | |
| 3634 | 2.3 | U12595 | Hs 2204 | Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds |
| 4674 | 2.3 | U54099 | Hs 93121 | Human LGN protein mRNA complete cds |
| 5769 | 2.3 | X53500 | Hs 89690 | GRO3 oncogene |
| 25050 | 2.3 | AA011134 | Hs 25953 | ESTs Weakly similar to retin [H sapiens] |
| 41935 | 2.3 | T29681 | Hs 75761 | Human serine kinase mRNA complete cds |
| 26895 | 2.3 | AA392765 | Hs 42650 | H sapiens mRNA for M-phase phosphoprotein mpp5 |
| 1782 | 2.1 | L12711 | Hs 69643 | Transferrinase (Wernicke-Korsakoff syndrome) |
| 25593 | 2.1 | AA113149 | Hs 8130 | Homo sapiens IPL (IPL) mRNA complete cds |
| 1487 | 1.8 | J03934 | Hs 60706 | NAD(P)H:flavinone oxidoreductase |
| 7656 | 1.5 | AA203428 | Hs 7756 | ESTs Moderately similar to ANKTRN BRAIN VARIANT 2 [Homo sapiens] |
| 663 | 1.5 | D19997 | Hs 41097 | Human mRNA for KIAA0175 gene complete cds |
| 836 | 1.5 | D87444 | Hs 75305 | Human mRNA for KIAA0255 gene complete cds |
| 3098 | 1.2 | M7636 | Hs 79217 | PYRROLINE-5-CARBOXYLATE REDUCTASE |
| 6679 | 1.1 | Z25066 | Hs 50896 | H sapiens nck2 mRNA for protein kinase |
| 6880 | 1.0 | Z25067 | Hs 2236 | H sapiens nck2 mRNA for protein kinase |
| 2473 | 0.7 | M19304 | Hs 79748 | Antigen identified by monoclonal antibodies 4F2 TRA1 10 TROP4 and T43 |
| 36506 | 0.7 | AA429621 | Hs 75053 | Human 100 kDa coactivator mRNA complete cds |

FIGURE 2

| Primary Key | fold upregulated in Tumor | Accession | Unigene CLUSTER | Unigene Descriptor |
|-------------|---------------------------|---------------|---------------------|--|
| 33616 | >10 | W83726 | Hs.55279 | Protease inhibitor 5 (maspin) |
| 34197 | >10 | AA323315 | Hs.12540 | Human sapiens clone Z3797 and 23017 mRNA, partial cds |
| 19387 | >10 | H20128 | Hs.31656 | ESTs |
| 8125 | >10 | AA330771 | Hs.82911 | Human protein-tyrosine phosphatase (HLPP-1) mRNA, partial sequence |
| 18352 | >10 | AA222912 | Hs.12013 | Ribonuclease L (2'-5'-oligoadenylate synthetase-dependent) inhibitor |
| 39995 | >10 | H82474 | Hs.108240 | EST |
| 19328 | >10 | H17808 | Hs.22859 | ESTs |
| 38590 | >10 | AA598648 | Hs.78202 | Human mRNA for transcriptional activator hSNF2b complete cds |
| 38456 | >10 | AA504343 | Hs.101074 | ESTs |
| 17559 | >10 | AA129407 | Hs.11190 | ESTs |
| 5619 | >10 | X14859 | Hs.27111 | HISTONE H2A.X |
| 4029 | >10 | U21090 | Hs.14588 | Human DNA polymerase delta small subunit mRNA, complete cds |
| 15005 | >10 | U30246 | Hs.110736 | Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds |
| 3550 | >10 | U04313 | Hs.55279 | Protease inhibitor 5 (maspin) |
| 28916 | >10 | AA331393 | Hs.47378 | ESTs |
| 1346 | >10 | HG4716-HT5158 | EST - HG4716-HT5158 | ESTs highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans] |
| 37491 | 10.0 | AA45239 | Hs.07630 | ESTs highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans] |
| 13110 | 9.8 | AA433940 | Hs.19114 | Human sapiens mRNA for high mobility group protein HMG2a |
| 4876 | 9.8 | U55206 | Hs.78619 | Human sapiens human gamma-glutamyl hydrolase (IGH) mRNA complete cds |
| 21655 | 8.7 | R38239 | Hs.25276 | EST |
| 14723 | 8.3 | D59094 | Hs.34782 | ESTs |
| 5793 | 7.4 | X54942 | Hs.03758 | CDC28 protein kinase 2 |
| 29648 | 7.1 | N22107 | Hs.124215 | ESTs |
| 3947 | 7.0 | H03866 | Hs.112013 | ESTs |
| 6078 | 7.0 | X89141 | Hs.18276 | FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE |
| 9326 | 6.8 | D89377 | Hs.09404 | Msh (Drosophila) homeo box homolog 2 |
| 1566 | 6.7 | J05614 | EST - J05614 | ESTs highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus] |
| 25575 | 6.7 | AA129757 | Hs.54602 | ESTs |
| 20126 | 6.4 | N22015 | Hs.18457 | ESTs |
| 6051 | 6.1 | X89314 | Hs.2704 | Galectin peroxidase 2 gastrointestinal |
| 10887 | 5.1 | AA084458 | Hs.19322 | ESTs Weakly similar to "LU SURFAMILY 1" |
| 18092 | 5.0 | AA179845 | Hs.78625 | ESTs Moderately similar to rablinsin-6 [IM musculus] |
| 4093 | 5.0 | U25182 | Hs.03363 | Human antioxidant enzyme AOE37-2 mRNA complete cds |
| 18290 | 5.8 | AA211901 | Hs.86430 | ESTs |
| 5330 | 5.8 | U91327 | EST - U91327 | Human chromosome segregation gene homolog CAS mRNA complete cds |
| 4244 | 5.7 | U33286 | Hs.90073 | Human chromosome segregation gene homolog CAS mRNA complete cds |

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FIGURE 2 (CONT.)

| | | | | |
|-------|----|---------------|----------------------|--|
| 6928 | 57 | Z46529 | Hs.2316 | SRY (sex-determining region Y) box 9 (campomelic dysplasia autosomal sex-reversal) |
| 6180 | 56 | X74794 | Hs.69599 | CD221 HOMOLOG |
| 31487 | 54 | N69507 | Hs.12949 | ESTs |
| 9470 | 53 | H46817 | EST - H46617 | |
| 33450 | 50 | V96835 | Hs.14150 | Homo sapiens mRNA for KIAA0036 protein, complete cds |
| 12689 | 50 | | Hs.5101 | Homo sapiens protein regulating cytokinesis 1 (PRC1)mRNA, complete cds |
| 11106 | 48 | HQ2381-173127 | EST - HC2081-HT3127 | |
| 34367 | 48 | A4251758 | Hs.40323 | Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds |
| 11595 | 48 | A4242819 | Hs.32539 | ESTs |
| 17622 | 48 | A4131594 | Hs.71435 | ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae] |
| 34754 | 47 | A4287642 | Hs.81948 | Human mRNA for KIAA0076 gene, complete cds |
| 25038 | 47 | A4010065 | Hs.83759 | CD226 protein kinase 2 |
| 5312 | 46 | U09716 | Hs.70187 | Human cell surface protein NCAR mRNA, complete cds |
| 8095 | 46 | A3314779 | Hs.105484 | ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H. sapiens] |
| 33656 | 46 | V95477 | Hs.50662 | ESTs |
| 8284 | 45 | A4401334 | Hs.106941 | ESTs |
| 34479 | 45 | A4362080 | Hs.110736 | Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds |
| 7898 | 44 | A4263032 | Hs.81634 | ESTs |
| 10716 | 44 | A4053319 | Hs.9951 | ESTs |
| 5680 | 44 | X17020 | Hs.118538 | NUCLEOSIDE DIPHOSPHATE KINASE A |
| 20203 | 43 | N26855 | Hs.3688 | ESTs Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY [III [H. sapiens] |
| 10823 | 42 | A4116036 | Hs.9329 | ESTs |
| 20050 | 41 | A4479139 | Hs.75393 | Acid phosphatase 1 soluble |
| 10970 | 41 | A4129390 | Hs.5285 | ESTs |
| 4149 | 41 | U25386 | Hs.2397 | RAG (recombination activating gene) cshort 1 |
| 5767 | 41 | X53793 | Hs.118226 | MULTIFUNCTIONAL PROTEIN ADE2 |
| 26596 | 40 | A4279943 | Hs.80971 | ESTs |
| 9961 | 39 | AFXX- | AFXX HI MTFRM11507_3 | |
| 38604 | 39 | A4598603 | Hs.114496 | ESTs |
| 30560 | 39 | N49284 | Hs.1334 | MYB PROTO-ONCOGENE PROTEIN |
| 8513 | 38 | A4446990 | Hs.103135 | ESTs |
| 14509 | 38 | A4609943 | Hs.32793 | ESTs |
| 25284 | 38 | A4045074 | Hs.110146 | ESTs Weakly similar to 52-KD SS-A/Ro autoantigen [H. sapiens] |
| 27354 | 38 | AA425221 | Hs.81688 | ESTs |
| 18385 | 38 | A4227219 | Hs.110626 | Homo sapiens CAGF9 mRNA, partial cds |
| 25240 | 37 | A4039713 | Hs.110406 | ESTs |
| 16854 | 37 | A4055552 | Hs.71622 | ESTs Weakly similar to KIAA0319 [H. sapiens] |
| 3769 | 37 | U07550 | Hs.11197 | Heat shock 10 KD protein 1 (chaperonin 10) |
| 13806 | 35 | AA456437 | Hs.20366 | ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H. sapiens] |
| 8338 | 34 | AA417152 | Hs.51101 | Homo sapiens protein regulating cytokinesis 1 (PRC1)mRNA, complete cds |

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FIGURE 2 (CONT.)

| | | | |
|-------|----------|-------------------|--|
| 387 | D26589 | EST - D26589 | ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus] |
| 15643 | W88247 | Hs.27437 | ESTs |
| 13838 | AA465342 | Hs.34045 | Basic transcription element binding protein 2 |
| 251 | D14520 | Hs.84728 | Zinc finger protein 139 (clone pHz-37) |
| 3778 | U03648 | Hs.363 | AD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE |
| 5660 | X16396 | Hs.37791 | ESTs |
| 17365 | AA101551 | Hs.68900 | Human sapiens importin beta subunit mRNA, complete cds |
| 33965 | AA181550 | Hs.81690 | ESTs |
| 1823 | H12634 | Hs.8104 | ESTs |
| 13767 | AA463234 | Hs.116387 | ESTs |
| 4738 | U59766 | Hs.75801 | Human FX protein mRNA, complete cds |
| 17041 | AA070384 | EST - RC_AA070384 | ESTs |
| 15504 | U29362 | Hs.44131 | Human translation initiation factor eIF3 p65 subunit mRNA, complete cds |
| 7401 | U0364800 | Hs.55692 | ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus] |
| 18693 | F04269 | Hs.56404 | ESTs Weakly similar to IIR ALU SUBFAMILY C |
| 23830 | T06600 | Hs.725723 | ESTs |
| 11288 | AA108512 | Hs.26910 | Thymidylate synthase |
| 170 | D03586 | Hs.02662 | ESTs |
| 11659 | AA231609 | Hs.35708 | Human sapiens MAD3-like protein kinase mRNA, complete cds |
| 14134 | AA465060 | Hs.3568 | ESTs Highly similar to phosphorylation regulatory protein HP-10 [H. sapiens] |
| 11140 | AA136132 | Hs.11817 | ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae] |
| 17625 | AA164209 | Hs.31730 | Human sapiens RRM RNA binding protein Gy-fbp (GRY-RBP) mRNA, complete cds |
| 26530 | AA278600 | Hs.73291 | ESTs |
| 7445 | AA104023 | Hs.110048 | ESTs |
| 18035 | AA175337 | Hs.73596 | ESTs |
| 15174 | U02897 | Hs.87246 | Human Bcl-2 binding component 3 (bcl-3) mRNA, partial cds |
| 33620 | W93843 | Hs.59509 | ESTs |
| 1932 | L24504 | Hs.75539 | Human (p23) mRNA, complete cds |
| 39556 | F03738 | Hs.3657 | ESTs |
| 1605 | U00058 | Hs.78070 | V-myc avian myelocytomatosis viral oncogene homolog |
| 4436 | U48705 | Hs.75562 | Receptor protein-tyrosine kinase EDDR1 |
| 36200 | AA421164 | Hs.107213 | ESTs |
| 12313 | AA397916 | Hs.22595 | ESTs |
| 18957 | H61476 | Hs.15641 | ESTs |
| 6081 | X69358 | Hs.82685 | CD47 antigen (Rb-related antigen integrin-associated signal transducer) |
| 16708 | AA043944 | Hs.62663 | ESTs |
| 357 | D26156 | Hs.78202 | Human mRNA for transcriptional activator NSNF2b, complete cds |
| 8059 | AA310967 | Hs.5090 | ESTs Weakly similar to T0448.11 [C.elegans] |
| 35830 | AA411448 | Hs.193986 | ESTs |
| 20151 | N22955 | Hs.6831 | Human sapiens clone 1400 unknown protein mRNA, partial cds |

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FIGURE 2 (CONT.)

| | | | | | |
|-------|----------|-----|-----------|--|--|
| 28258 | AA505133 | 2,8 | Hs.52273 | ESTs | |
| 8816 | AA460077 | 2,8 | Hs.29555 | ESTs | |
| 6480 | X91788 | 2,8 | Hs.94974 | H.sapiens mRNA for lcn protein | |
| 14566 | AA521122 | 2,8 | Hs.5196 | ESTs | |
| 14182 | AA490085 | 2,8 | Hs.21768 | ESTs | |
| 35955 | AA412528 | 2,7 | Hs.20183 | ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [R.norvegicus] | |
| 17842 | AA132883 | 2,7 | Hs.44155 | ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H.sapiens] | |
| 6131 | X72841 | 2,7 | Hs.2789 | Human retinoblastoma-binding protein (RbAp48) mRNA complete cds | |
| 6444 | X69750 | 2,7 | Hs.30077 | H.sapiens mRNA for TGF protein | |
| 7701 | AA215333 | 2,7 | Hs.97101 | ESTs | |
| 42554 | X73159 | 2,7 | Hs.88403 | Homo sapiens protein-tyrosine kinase EphB2v (EPHB2) mRNA complete cds | |
| 34768 | AA281259 | 2,7 | Hs.97101 | ESTs | |
| 1923 | X23806 | 2,7 | Hs.1895 | Matrix metalloproteinase 12 (macrophage elastase) | |
| 11305 | AA126719 | 2,6 | Hs.25282 | ESTs | |
| 4086 | AA207114 | 2,6 | Hs.27842 | ESTs | |
| 5587 | U22704 | 2,6 | Hs.111709 | Human antileukotriene factor-1 mRNA complete cds | |
| 19841 | X13482 | 2,6 | Hs.80506 | U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' | |
| 7614 | H59617 | 2,6 | Hs.5196 | ESTs Highly similar to UBQUITIN-CONJUGATING ENZYME E2-17 KD [Drosophila melanogaster] | |
| 11962 | AA197579 | 2,6 | Hs.102696 | ESTs Weakly similar to Yel007c-ap [S.cerevisiae] | |
| 13866 | AA227281 | 2,6 | Hs.20622 | ESTs | |
| 2893 | AA476319 | 2,6 | Hs.5327 | ESTs | |
| 12866 | M64929 | 2,6 | Hs.75200 | Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform | |
| 5932 | AA430032 | 2,6 | Hs.7487 | ESTs Moderately similar to PTTG gene product [R.norvegicus] | |
| 35434 | X62153 | 2,5 | Hs.82479 | Minichromosome maintenance deficient (S. cerevisiae) 3 | |
| 38185 | AA457013 | 2,5 | Hs.142592 | ESTs | |
| 1424 | AA467508 | 2,5 | Hs.9477 | Homo sapiens mRNA for KIAA0688 protein complete cds | |
| 21976 | J02645 | 2,5 | Hs.81613 | Eukaryotic translation initiation factor 2A | |
| 6485 | R43286 | 2,5 | Hs.75914 | EST - RC_R43286 | |
| 7980 | X92098 | 2,4 | Hs.8532 | H.sapiens mRNA for transmembrane protein mp24 | |
| 452 | AA282277 | 2,4 | Hs.8532 | Homo sapiens brain expressed ring finger protein mRNA complete cds | |
| 11701 | D3076 | 2,4 | Hs.24763 | RAN binding protein 1 | |
| 35390 | AA253031 | 2,4 | Hs.31730 | Homo sapiens RRM RNA binding protein Gpy-bp (GPy-RBP) mRNA complete cds | |
| 14420 | AA426291 | 2,4 | Hs.108527 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 6387 | AA460322 | 2,4 | Hs.19574 | ESTs Highly similar to AAC-RICH1 MRNA CLONE ACG3 PROTEIN [Dicyostelium discoidium] | |
| 1497 | X65372 | 2,4 | Hs.104195 | H.sapiens mRNA for Sm protein F | |
| 27672 | J04088 | 2,4 | Hs.3378 | Topoisomerase (DNA) II alpha (170kD) | |
| 8163 | AA459254 | 2,4 | Hs.48955 | ESTs | |
| 23965 | AA357394 | 2,4 | Hs.98073 | ESTs | |
| 20837 | T24539 | 2,4 | Hs.7165 | ESTs Highly similar to zinc finger protein [M.musculus] | |
| | | 2,4 | Hs.20624 | ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens] | |

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FIGURE 2 (CONT.)

| | | | | | |
|-------|-----|---------------|-----------|------|---|
| 17352 | 2,3 | AA100925 | Hs.20990 | ESTs | EST - RC_D51272_s |
| 28796 | 2,3 | D51272 | Hs.4310 | ESTs | |
| 28679 | 2,3 | AA281733 | Hs.14611 | ESTs | Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds |
| 24092 | 2,3 | W42845 | Hs.83532 | ESTs | Membrane cofactor protein (CD46) topoblast-lymphocyte cross-reactive antigen) |
| 4975 | 2,3 | X52405 | Hs.7381 | ESTs | Homo sapiens voltage dependent anion channel protein mRNA complete cds |
| 7404 | 2,3 | AA091939 | Hs.77168 | ESTs | Homo sapiens mRNA for Sm protein G |
| 6398 | 2,3 | X65273 | Hs.25863 | ESTs | ESTs Weakly similar to retin [H.sapiens] |
| 6398 | 2,3 | AA011134 | Hs.75761 | ESTs | Human serine kinase mRNA complete cds |
| 41905 | 2,3 | T26881 | Hs.21486 | ESTs | SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA |
| 3343 | 2,3 | M87936 | Hs.80684 | ESTs | High-mobility group (nucleosome chromosomal) protein 2 |
| 9937 | 2,2 | X62534 | Hs.5683 | ESTs | Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds |
| 20843 | 2,2 | X62534 | Hs.76887 | ESTs | Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds |
| 28448 | 2,2 | N69352 | Hs.1475 | ESTs | EST - D78129 |
| 651 | 2,2 | D76129 | Hs.103300 | ESTs | Homo sapiens diphthamide biosynthesis protein-2 (DPH2) mRNA complete cds |
| 11688 | 2,2 | AA252672 | Hs.21214 | ESTs | |
| 11603 | 2,2 | AA257971 | Hs.1334 | ESTs | MYB PROTO-ONCOGENE PROTEIN |
| 4046 | 2,2 | U22376 | Hs.27831 | ESTs | |
| 20276 | 2,2 | N32919 | Hs.10058 | ESTs | ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPY7 INTERGENIC REGION [Saccharomyces cerevisiae] |
| 3470 | 2,1 | AA251829 | Hs.10600 | ESTs | ESTs Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae] |
| 14592 | 2,1 | AA621340 | Hs.10600 | ESTs | EST - S75256 |
| 3461 | 2,1 | S75256 | Hs.10600 | ESTs | EST - HG1112-HT1112 |
| 524 | 2,1 | HG1112-HT1112 | Hs.77989 | ESTs | Topomyosin alpha chain (skeletal muscle) |
| 24348 | 2,1 | W66469 | Hs.15313 | ESTs | ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BIRC [S. cerevisiae] |
| 10098 | 2,1 | AA112063 | Hs.78770 | ESTs | Isoleucine-tRNA synthetase |
| 361 | 2,1 | D28473 | Hs.10724 | ESTs | ESTs Weakly similar to unknown [S. cerevisiae] |
| 11528 | 2,1 | AA236018 | Hs.8130 | ESTs | Homo sapiens IPL (IPL) mRNA complete cds |
| 25593 | 2,1 | AA113149 | Hs.107213 | ESTs | |
| 38040 | 2,1 | AA481403 | Hs.83550 | ESTs | Human heterochromatin protein HP1-Hs-gamma mRNA complete cds |
| 4111 | 2,1 | U26312 | Hs.83379 | ESTs | Cyclochrome c oxidase subunit Vlb |
| 61 | 2,0 | AC002115 | Hs.83379 | ESTs | Coproporphyrinogen oxidase (coproporphyrin henderoporphyrin) |
| 5112 | 2,0 | D16611 | Hs.89866 | ESTs | EST - D28423 |
| 380 | 2,0 | D28423 | Hs.89866 | ESTs | EST - D28364 |
| 377 | 2,0 | D28364 | Hs.42392 | ESTs | |
| 28379 | 2,0 | AA608710 | Hs.5950 | ESTs | |
| 24230 | 2,0 | W72276 | Hs.9564 | ESTs | Human clone 121711 defective miniprep transposon Hsmar2 mRNA sequence |
| 40212 | 2,0 | H85535 | Hs.104558 | ESTs | |
| 8118 | 2,0 | AA328993 | Hs.104558 | ESTs | |

FIGURE 3

[illegible]

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FIGURE 3 (CONT.)

| | | | |
|--------|-------------|-----------|---|
| 4921 | UT3524 | Hs 87465 | Human putative ATP/GTP-binding protein (p85-JAR) mRNA, complete cds |
| 4922 | U03444 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 20158 | A0250179 | Hs 89131 | EST |
| 1455 | U03444 | Hs 14732 | MAL-1 GTP-BINDING PROTEIN |
| 8111 | A032717 | Hs 4770 | EST |
| 19389 | H02165 | Hs 31734 | EST |
| 39270 | A050749 | Hs 122309 | EST |
| 2119 | R07915 | Hs 122309 | Weakly similar to GTP-BINDING PROTEIN (p85-JAR) mRNA, complete cds |
| 4107 | R07915 | Hs 122309 | EST |
| 1980 | H02165 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 40494 | X01880 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 4102 | F04022 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 19676 | X01880 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 4137 | X01880 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 36465 | A034522 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 19320 | A034522 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 42786 | Z03034 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 34014 | A013344 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 29931 | R02023 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 1196 | A014299 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 1158 | G3344-H7351 | Hs 14635 | EST |
| 27374 | A014299 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 21156 | N03513 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 10902 | A035166 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 5199 | X54262 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 11962 | A035200 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 20057 | H02079 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 58448 | C02002 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 22578 | R02079 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 41307 | R02079 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 42011 | A014299 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 28030 | A014299 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 421364 | L47276 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 9127 | C02002 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 59614 | X01880 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 42586 | U04714 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 35598 | U04714 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |
| 35508 | A035060 | Hs 14635 | Human putative GTP-binding protein (p85-JAR) mRNA, complete cds |

[illegible]

| | | | |
|-------|----|---------|--|
| 20277 | 10 | NA10886 | Human myosin VIIb, non-disseminating protein, complete cds |
| 20278 | 10 | U03933 | Human myosin VIIb, non-disseminating protein, complete cds |
| 20279 | 10 | U03934 | Human myosin VIIb, non-disseminating protein, complete cds |
| 41340 | 10 | U13204 | EST: H13204. EST |
| 30981 | 10 | AA83550 | EST: H13204. EST |
| 30982 | 10 | AA83550 | EST: H13204. EST |
| 16598 | 10 | AA20261 | EST: H13204. EST |
| 41991 | 10 | U03848 | EST: H13204. EST |
| 41992 | 10 | U03848 | EST: H13204. EST |
| 20010 | 10 | AA17145 | EST: H13204. EST |
| 20011 | 10 | AA17145 | EST: H13204. EST |
| 40008 | 10 | U03824 | EST: H13204. EST |
| 40009 | 10 | U03824 | EST: H13204. EST |
| 1445 | 10 | J03027 | Human MHC class I protein, HLA-G |
| 12842 | 10 | AA44964 | U143131. EST |
| 37133 | 10 | AA44750 | U143131. EST |
| 42542 | 10 | T88979 | Human HLA-G gene, complete cds |
| 37134 | 10 | AA44750 | U143131. EST |
| 2141 | 10 | AA44943 | U143131. EST |
| 2142 | 10 | U03803 | U143131. EST |
| 2143 | 10 | U03803 | U143131. EST |
| 31953 | 10 | AA17320 | U143131. EST |
| 40901 | 10 | U03802 | U143131. EST |
| 40902 | 10 | U03802 | U143131. EST |
| 54571 | 10 | AA24212 | U143131. EST |
| 3639 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3640 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3641 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3642 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3643 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3644 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3645 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3646 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3647 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3648 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3649 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3650 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3651 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3652 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3653 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3654 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3655 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3656 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3657 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3658 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3659 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3660 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3661 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3662 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3663 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3664 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3665 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3666 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3667 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3668 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3669 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3670 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3671 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3672 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3673 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3674 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3675 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3676 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3677 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3678 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3679 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3680 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3681 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3682 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3683 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3684 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3685 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3686 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3687 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3688 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3689 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3690 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3691 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3692 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3693 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3694 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3695 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3696 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3697 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3698 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |
| 3699 | 10 | U03279 | Proteinase inhibitor 5 (resenin) |

FIGURE 3 (CONT.)

[illegible]

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[illegible]

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FIGURE 3 (CONT.)

[illegible]

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| | | | | |
|----|----------|----------|------|--|
| 77 | HA424534 | Ha 12415 | EST1 | |
| 77 | H03831 | Ha 12416 | EST1 | |
| 77 | HA424535 | Ha 12417 | EST1 | |
| 77 | HA424536 | Ha 12418 | EST1 | |
| 77 | HA424537 | Ha 12419 | EST1 | |
| 77 | HA424538 | Ha 12420 | EST1 | |
| 77 | HA424539 | Ha 12421 | EST1 | |
| 77 | HA424540 | Ha 12422 | EST1 | |
| 77 | HA424541 | Ha 12423 | EST1 | |
| 77 | HA424542 | Ha 12424 | EST1 | |
| 77 | HA424543 | Ha 12425 | EST1 | |
| 77 | HA424544 | Ha 12426 | EST1 | |
| 77 | HA424545 | Ha 12427 | EST1 | |
| 77 | HA424546 | Ha 12428 | EST1 | |
| 77 | HA424547 | Ha 12429 | EST1 | |
| 77 | HA424548 | Ha 12430 | EST1 | |
| 77 | HA424549 | Ha 12431 | EST1 | |
| 77 | HA424550 | Ha 12432 | EST1 | |
| 77 | HA424551 | Ha 12433 | EST1 | |
| 77 | HA424552 | Ha 12434 | EST1 | |
| 77 | HA424553 | Ha 12435 | EST1 | |
| 77 | HA424554 | Ha 12436 | EST1 | |
| 77 | HA424555 | Ha 12437 | EST1 | |
| 77 | HA424556 | Ha 12438 | EST1 | |
| 77 | HA424557 | Ha 12439 | EST1 | |
| 77 | HA424558 | Ha 12440 | EST1 | |
| 77 | HA424559 | Ha 12441 | EST1 | |
| 77 | HA424560 | Ha 12442 | EST1 | |
| 77 | HA424561 | Ha 12443 | EST1 | |
| 77 | HA424562 | Ha 12444 | EST1 | |
| 77 | HA424563 | Ha 12445 | EST1 | |
| 77 | HA424564 | Ha 12446 | EST1 | |
| 77 | HA424565 | Ha 12447 | EST1 | |
| 77 | HA424566 | Ha 12448 | EST1 | |
| 77 | HA424567 | Ha 12449 | EST1 | |
| 77 | HA424568 | Ha 12450 | EST1 | |
| 77 | HA424569 | Ha 12451 | EST1 | |
| 77 | HA424570 | Ha 12452 | EST1 | |
| 77 | HA424571 | Ha 12453 | EST1 | |
| 77 | HA424572 | Ha 12454 | EST1 | |
| 77 | HA424573 | Ha 12455 | EST1 | |
| 77 | HA424574 | Ha 12456 | EST1 | |
| 77 | HA424575 | Ha 12457 | EST1 | |
| 77 | HA424576 | Ha 12458 | EST1 | |
| 77 | HA424577 | Ha 12459 | EST1 | |
| 77 | HA424578 | Ha 12460 | EST1 | |
| 77 | HA424579 | Ha 12461 | EST1 | |
| 77 | HA424580 | Ha 12462 | EST1 | |
| 77 | HA424581 | Ha 12463 | EST1 | |
| 77 | HA424582 | Ha 12464 | EST1 | |
| 77 | HA424583 | Ha 12465 | EST1 | |
| 77 | HA424584 | Ha 12466 | EST1 | |
| 77 | HA424585 | Ha 12467 | EST1 | |
| 77 | HA424586 | Ha 12468 | EST1 | |
| 77 | HA424587 | Ha 12469 | EST1 | |
| 77 | HA424588 | Ha 12470 | EST1 | |
| 77 | HA424589 | Ha 12471 | EST1 | |
| 77 | HA424590 | Ha 12472 | EST1 | |
| 77 | HA424591 | Ha 12473 | EST1 | |
| 77 | HA424592 | Ha 12474 | EST1 | |
| 77 | HA424593 | Ha 12475 | EST1 | |
| 77 | HA424594 | Ha 12476 | EST1 | |
| 77 | HA424595 | Ha 12477 | EST1 | |
| 77 | HA424596 | Ha 12478 | EST1 | |
| 77 | HA424597 | Ha 12479 | EST1 | |
| 77 | HA424598 | Ha 12480 | EST1 | |
| 77 | HA424599 | Ha 12481 | EST1 | |
| 77 | HA424600 | Ha 12482 | EST1 | |
| 77 | HA424601 | Ha 12483 | EST1 | |
| 77 | HA424602 | Ha 12484 | EST1 | |
| 77 | HA424603 | Ha 12485 | EST1 | |
| 77 | HA424604 | Ha 12486 | EST1 | |
| 77 | HA424605 | Ha 12487 | EST1 | |
| 77 | HA424606 | Ha 12488 | EST1 | |
| 77 | HA424607 | Ha 12489 | EST1 | |
| 77 | HA424608 | Ha 12490 | EST1 | |
| 77 | HA424609 | Ha 12491 | EST1 | |
| 77 | HA424610 | Ha 12492 | EST1 | |
| 77 | HA424611 | Ha 12493 | EST1 | |
| 77 | HA424612 | Ha 12494 | EST1 | |
| 77 | HA424613 | Ha 12495 | EST1 | |
| 77 | HA424614 | Ha 12496 | EST1 | |
| 77 | HA424615 | Ha 12497 | EST1 | |
| 77 | HA424616 | Ha 12498 | EST1 | |
| 77 | HA424617 | Ha 12499 | EST1 | |
| 77 | HA424618 | Ha 12500 | EST1 | |
| 77 | HA424619 | Ha 12501 | EST1 | |

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FIGURE 3 (CONT.)

| | | | |
|-------|---------|----------|---|
| 29273 | AA12937 | Hs 54602 | ESTs highly similar to G22 RIBOSOMAL PROTEIN L22 [Ratia non-pang] |
| 29274 | AA12938 | Hs 54603 | Hs 54603 ESTs |
| 29275 | AA12939 | Hs 54604 | Hs 54604 ESTs |
| 29276 | AA12940 | Hs 54605 | Hs 54605 ESTs |
| 29277 | AA12941 | Hs 54606 | Hs 54606 ESTs |
| 29278 | AA12942 | Hs 54607 | Hs 54607 ESTs |
| 29279 | AA12943 | Hs 54608 | Hs 54608 ESTs |
| 29280 | AA12944 | Hs 54609 | Hs 54609 ESTs |
| 29281 | AA12945 | Hs 54610 | Hs 54610 ESTs |
| 29282 | AA12946 | Hs 54611 | Hs 54611 ESTs |
| 29283 | AA12947 | Hs 54612 | Hs 54612 ESTs |
| 29284 | AA12948 | Hs 54613 | Hs 54613 ESTs |
| 29285 | AA12949 | Hs 54614 | Hs 54614 ESTs |
| 29286 | AA12950 | Hs 54615 | Hs 54615 ESTs |
| 29287 | AA12951 | Hs 54616 | Hs 54616 ESTs |
| 29288 | AA12952 | Hs 54617 | Hs 54617 ESTs |
| 29289 | AA12953 | Hs 54618 | Hs 54618 ESTs |
| 29290 | AA12954 | Hs 54619 | Hs 54619 ESTs |
| 29291 | AA12955 | Hs 54620 | Hs 54620 ESTs |
| 29292 | AA12956 | Hs 54621 | Hs 54621 ESTs |
| 29293 | AA12957 | Hs 54622 | Hs 54622 ESTs |
| 29294 | AA12958 | Hs 54623 | Hs 54623 ESTs |
| 29295 | AA12959 | Hs 54624 | Hs 54624 ESTs |
| 29296 | AA12960 | Hs 54625 | Hs 54625 ESTs |
| 29297 | AA12961 | Hs 54626 | Hs 54626 ESTs |
| 29298 | AA12962 | Hs 54627 | Hs 54627 ESTs |
| 29299 | AA12963 | Hs 54628 | Hs 54628 ESTs |
| 29300 | AA12964 | Hs 54629 | Hs 54629 ESTs |
| 29301 | AA12965 | Hs 54630 | Hs 54630 ESTs |
| 29302 | AA12966 | Hs 54631 | Hs 54631 ESTs |
| 29303 | AA12967 | Hs 54632 | Hs 54632 ESTs |
| 29304 | AA12968 | Hs 54633 | Hs 54633 ESTs |
| 29305 | AA12969 | Hs 54634 | Hs 54634 ESTs |
| 29306 | AA12970 | Hs 54635 | Hs 54635 ESTs |
| 29307 | AA12971 | Hs 54636 | Hs 54636 ESTs |
| 29308 | AA12972 | Hs 54637 | Hs 54637 ESTs |
| 29309 | AA12973 | Hs 54638 | Hs 54638 ESTs |
| 29310 | AA12974 | Hs 54639 | Hs 54639 ESTs |
| 29311 | AA12975 | Hs 54640 | Hs 54640 ESTs |
| 29312 | AA12976 | Hs 54641 | Hs 54641 ESTs |
| 29313 | AA12977 | Hs 54642 | Hs 54642 ESTs |
| 29314 | AA12978 | Hs 54643 | Hs 54643 ESTs |
| 29315 | AA12979 | Hs 54644 | Hs 54644 ESTs |
| 29316 | AA12980 | Hs 54645 | Hs 54645 ESTs |
| 29317 | AA12981 | Hs 54646 | Hs 54646 ESTs |
| 29318 | AA12982 | Hs 54647 | Hs 54647 ESTs |
| 29319 | AA12983 | Hs 54648 | Hs 54648 ESTs |
| 29320 | AA12984 | Hs 54649 | Hs 54649 ESTs |
| 29321 | AA12985 | Hs 54650 | Hs 54650 ESTs |
| 29322 | AA12986 | Hs 54651 | Hs 54651 ESTs |
| 29323 | AA12987 | Hs 54652 | Hs 54652 ESTs |
| 29324 | AA12988 | Hs 54653 | Hs 54653 ESTs |
| 29325 | AA12989 | Hs 54654 | Hs 54654 ESTs |
| 29326 | AA12990 | Hs 54655 | Hs 54655 ESTs |
| 29327 | AA12991 | Hs 54656 | Hs 54656 ESTs |
| 29328 | AA12992 | Hs 54657 | Hs 54657 ESTs |
| 29329 | AA12993 | Hs 54658 | Hs 54658 ESTs |
| 29330 | AA12994 | Hs 54659 | Hs 54659 ESTs |
| 29331 | AA12995 | Hs 54660 | Hs 54660 ESTs |
| 29332 | AA12996 | Hs 54661 | Hs 54661 ESTs |
| 29333 | AA12997 | Hs 54662 | Hs 54662 ESTs |
| 29334 | AA12998 | Hs 54663 | Hs 54663 ESTs |
| 29335 | AA12999 | Hs 54664 | Hs 54664 ESTs |
| 29336 | AA13000 | Hs 54665 | Hs 54665 ESTs |
| 29337 | AA13001 | Hs 54666 | Hs 54666 ESTs |
| 29338 | AA13002 | Hs 54667 | Hs 54667 ESTs |
| 29339 | AA13003 | Hs 54668 | Hs 54668 ESTs |
| 29340 | AA13004 | Hs 54669 | Hs 54669 ESTs |
| 29341 | AA13005 | Hs 54670 | Hs 54670 ESTs |
| 29342 | AA13006 | Hs 54671 | Hs 54671 ESTs |
| 29343 | AA13007 | Hs 54672 | Hs 54672 ESTs |
| 29344 | AA13008 | Hs 54673 | Hs 54673 ESTs |
| 29345 | AA13009 | Hs 54674 | Hs 54674 ESTs |
| 29346 | AA13010 | Hs 54675 | Hs 54675 ESTs |
| 29347 | AA13011 | Hs 54676 | Hs 54676 ESTs |
| 29348 | AA13012 | Hs 54677 | Hs 54677 ESTs |
| 29349 | AA13013 | Hs 54678 | Hs 54678 ESTs |
| 29350 | AA13014 | Hs 54679 | Hs 54679 ESTs |
| 29351 | AA13015 | Hs 54680 | Hs 54680 ESTs |
| 29352 | AA13016 | Hs 54681 | Hs 54681 ESTs |
| 29353 | AA13017 | Hs 54682 | Hs 54682 ESTs |
| 29354 | AA13018 | Hs 54683 | Hs 54683 ESTs |
| 29355 | AA13019 | Hs 54684 | Hs 54684 ESTs |
| 29356 | AA13020 | Hs 54685 | Hs 54685 ESTs |
| 29357 | AA13021 | Hs 54686 | Hs 54686 ESTs |
| 29358 | AA13022 | Hs 54687 | Hs 54687 ESTs |
| 29359 | AA13023 | Hs 54688 | Hs 54688 ESTs |
| 29360 | AA13024 | Hs 54689 | Hs 54689 ESTs |
| 29361 | AA13025 | Hs 54690 | Hs 54690 ESTs |
| 29362 | AA13026 | Hs 54691 | Hs 54691 ESTs |
| 29363 | AA13027 | Hs 54692 | Hs 54692 ESTs |
| 29364 | AA13028 | Hs 54693 | Hs 54693 ESTs |
| 29365 | AA13029 | Hs 54694 | Hs 54694 ESTs |
| 29366 | AA13030 | Hs 54695 | Hs 54695 ESTs |
| 29367 | AA13031 | Hs 54696 | Hs 54696 ESTs |
| 29368 | AA13032 | Hs 54697 | Hs 54697 ESTs |
| 29369 | AA13033 | Hs 54698 | Hs 54698 ESTs |
| 29370 | AA13034 | Hs 54699 | Hs 54699 ESTs |
| 29371 | AA13035 | Hs 54700 | Hs 54700 ESTs |
| 29372 | AA13036 | Hs 54701 | Hs 54701 ESTs |
| 29373 | AA13037 | Hs 54702 | Hs 54702 ESTs |
| 29374 | AA13038 | Hs 54703 | Hs 54703 ESTs |
| 29375 | AA13039 | Hs 54704 | Hs 54704 ESTs |
| 29376 | AA13040 | Hs 54705 | Hs 54705 ESTs |
| 29377 | AA13041 | Hs 54706 | Hs 54706 ESTs |
| 29378 | AA13042 | Hs 54707 | Hs 54707 ESTs |
| 29379 | AA13043 | Hs 54708 | Hs 54708 ESTs |
| 29380 | AA13044 | Hs 54709 | Hs 54709 ESTs |
| 29381 | AA13045 | Hs 54710 | Hs 54710 ESTs |
| 29382 | AA13046 | Hs 54711 | Hs 54711 ESTs |
| 29383 | AA13047 | Hs 54712 | Hs 54712 ESTs |
| 29384 | AA13048 | Hs 54713 | Hs 54713 ESTs |
| 29385 | AA13049 | Hs 54714 | Hs 54714 ESTs |
| 29386 | AA13050 | Hs 54715 | Hs 54715 ESTs |
| 29387 | AA13051 | Hs 54716 | Hs 54716 ESTs |
| 29388 | AA13052 | Hs 54717 | Hs 54717 ESTs |
| 29389 | AA13053 | Hs 54718 | Hs 54718 ESTs |
| 29390 | AA13054 | Hs 54719 | Hs 54719 ESTs |
| 29391 | AA13055 | Hs 54720 | Hs 54720 ESTs |
| 29392 | AA13056 | Hs 54721 | Hs 54721 ESTs |
| 29393 | AA13057 | Hs 54722 | Hs 54722 ESTs |
| 29394 | AA13058 | Hs 54723 | Hs 54723 ESTs |
| 29395 | AA13059 | Hs 54724 | Hs 54724 ESTs |
| 29396 | AA13060 | Hs 54725 | Hs 54725 ESTs |
| 29397 | AA13061 | Hs 54726 | Hs 54726 ESTs |
| 29398 | AA13062 | Hs 54727 | Hs 54727 ESTs |
| 29399 | AA13063 | Hs 54728 | Hs 54728 ESTs |
| 29400 | AA13064 | Hs 54729 | Hs 54729 ESTs |
| 29401 | AA13065 | Hs 54730 | Hs 54730 ESTs |
| 29402 | AA13066 | Hs 54731 | Hs 54731 ESTs |
| 29403 | AA13067 | Hs 54732 | Hs 54732 ESTs |
| 29404 | AA13068 | Hs 54733 | Hs 54733 ESTs |
| 29405 | AA13069 | Hs 54734 | Hs 54734 ESTs |
| 29406 | AA13070 | Hs 54735 | Hs 54735 ESTs |
| 29407 | AA13071 | Hs 54736 | Hs 54736 ESTs |
| 29408 | AA13072 | Hs 54737 | Hs 54737 ESTs |
| 29409 | AA13073 | Hs 54738 | Hs 54738 ESTs |
| 29410 | AA13074 | Hs 54739 | Hs 54739 ESTs |
| 29411 | AA13075 | Hs 54740 | Hs 54740 ESTs |
| 29412 | AA13076 | Hs 54741 | Hs 54741 ESTs |
| 29413 | AA13077 | Hs 54742 | Hs 54742 ESTs |
| 29414 | AA13078 | Hs 54743 | Hs 54743 ESTs |
| 29415 | AA13079 | Hs 54744 | Hs 54744 ESTs |
| 29416 | AA13080 | Hs 54745 | Hs 54745 ESTs |
| 29417 | AA13081 | Hs 54746 | Hs 54746 ESTs |
| 29418 | AA13082 | Hs 54747 | Hs 54747 ESTs |
| 29419 | AA13083 | Hs 54748 | Hs 54748 ESTs |
| 29420 | AA13084 | Hs 54749 | Hs 54749 ESTs |
| 29421 | AA13085 | Hs 54750 | Hs 54750 ESTs |
| 29422 | AA13086 | Hs 54751 | Hs 54751 ESTs |
| 29423 | AA13087 | Hs 54752 | Hs 54752 ESTs |
| 29424 | AA13088 | Hs 54753 | Hs 54753 ESTs |
| 29425 | AA13089 | Hs 54754 | Hs 54754 ESTs |
| 29426 | AA13090 | Hs 54755 | Hs 54755 ESTs |
| 29427 | AA13091 | Hs 54756 | Hs 54756 ESTs |
| 29428 | AA13092 | Hs 54757 | Hs 54757 ESTs |
| 29429 | AA13093 | Hs 54758 | Hs 54758 ESTs |
| 29430 | AA13094 | Hs 54759 | Hs 54759 ESTs |
| 29431 | AA13095 | Hs 54760 | Hs 54760 ESTs |
| 29432 | AA13096 | Hs 54761 | Hs 54761 ESTs |
| 29433 | AA13097 | Hs 54762 | Hs 54762 ESTs |
| 29434 | AA13098 | Hs 54763 | Hs 54763 ESTs |
| 29435 | AA13099 | Hs 54764 | Hs 54764 ESTs |
| 29436 | AA13100 | Hs 54765 | Hs 54765 ESTs |
| 29437 | AA13101 | Hs 54766 | Hs 54766 ESTs |
| 29438 | AA13102 | Hs 54767 | Hs 54767 ESTs |
| 29439 | AA13103 | Hs 54768 | Hs 54768 ESTs |
| 29440 | AA13104 | Hs 54769 | Hs 54769 ESTs |
| 29441 | AA13105 | Hs 54770 | Hs 54770 ESTs |
| 29442 | AA13106 | Hs 54771 | Hs 54771 ESTs |
| 29443 | AA13107 | Hs 54772 | Hs 54772 ESTs |
| 29444 | AA13108 | Hs 54773 | Hs 54773 ESTs |
| 29445 | AA13109 | Hs 54774 | Hs 54774 ESTs |
| 29446 | AA13110 | Hs 54775 | Hs 54775 ESTs |
| 29447 | AA13111 | Hs 54776 | Hs 54776 ESTs |
| 29448 | AA13112 | Hs 54777 | Hs 54777 ESTs |
| 29449 | AA13113 | Hs 54778 | Hs 54778 ESTs |
| 29450 | AA13114 | Hs 54779 | Hs 54779 ESTs |
| 29451 | AA13115 | Hs 54780 | Hs 54780 ESTs |
| 29452 | AA13116 | Hs 54781 | Hs 54781 ESTs |
| 29453 | AA13117 | Hs 54782 | Hs 54782 ESTs |
| 29454 | AA13118 | Hs 54783 | Hs 54783 ESTs |
| 29455 | AA13119 | Hs 54784 | Hs 54784 ESTs |
| 29456 | AA13120 | Hs 54785 | Hs 54785 ESTs |
| 29457 | AA13121 | Hs 54786 | Hs 54786 ESTs |
| 29458 | AA13122 | Hs 54787 | Hs 54787 ESTs |
| 29459 | AA13123 | Hs 54788 | Hs 54788 ESTs |
| 29460 | AA13124 | Hs 54789 | Hs 54789 ESTs |
| 29461 | AA13125 | Hs 54790 | Hs 54790 ESTs |
| 29462 | AA13126 | Hs 54791 | Hs 54791 ESTs |
| 29463 | AA13127 | Hs 54792 | Hs 54792 ESTs |
| 29464 | AA13128 | Hs 54793 | Hs 54793 ESTs |
| 29465 | AA13129 | Hs 54794 | Hs 54794 ESTs |
| 29466 | AA13130 | Hs 54795 | Hs 54795 ESTs |
| 29467 | AA13131 | Hs 54796 | Hs 54796 ESTs |
| 29468 | AA13132 | Hs 54797 | Hs 54797 ESTs |
| 29469 | AA13133 | Hs 54798 | Hs 54798 ESTs |
| 29470 | AA13134 | Hs 54799 | Hs 54799 ESTs |
| 29471 | AA13135 | Hs 54800 | Hs 54800 ESTs |
| 29472 | AA13136 | Hs 54801 | Hs 54801 ESTs |
| 29473 | AA13137 | Hs 54802 | Hs 54802 ESTs |
| 29474 | AA13138 | Hs 54803 | Hs 54803 ESTs |
| 29475 | AA13139 | Hs 54804 | Hs 54804 ESTs |
| 29476 | AA13140 | Hs 54805 | Hs 54805 ESTs |
| 29477 | AA13141 | Hs 54806 | Hs 54806 ESTs |
| 29478 | AA13142 | Hs 54807 | Hs 54807 ESTs |
| 29479 | AA13143 | Hs 54808 | Hs 54808 ESTs |
| 29480 | AA13144 | Hs 54809 | Hs 54809 ESTs |
| 29481 | AA13145 | Hs 54810 | Hs 54810 ESTs |
| 29482 | AA13146 | Hs 54811 | Hs 54811 ESTs |
| 29483 | AA13147 | Hs 54812 | Hs 54812 ESTs |
| 29484 | AA13148 | Hs 54813 | Hs 54813 ESTs |
| 29485 | AA13149 | Hs 54814 | Hs 54814 ESTs |
| 29486 | AA13150 | Hs 54815 | Hs 54815 ESTs |
| 29487 | AA13151 | Hs 54816 | Hs 54816 ESTs |
| 29488 | AA13152 | Hs 54817 | Hs 54817 ESTs |
| 29489 | AA13153 | Hs 54818 | Hs 54818 ESTs |
| 29490 | AA13154 | Hs 54819 | Hs 54819 ESTs |
| 29491 | AA13155 | Hs 54820 | Hs 54820 ESTs |
| 29492 | AA13156 | Hs 54821 | Hs 54821 ESTs |
| 29493 | AA13157 | Hs 54822 | Hs 54822 ESTs |
| 29494 | AA13158 | Hs 54823 | Hs 54823 ESTs |
| 29495 | AA13159 | Hs 54824 | Hs 54824 ESTs |
| 29496 | AA13160 | Hs 54825 | Hs 54825 ESTs |
| 29497 | AA13161 | Hs 54826 | Hs 54826 ESTs |
| 29498 | AA13162 | Hs 54827 | Hs 54827 ESTs |
| 29499 | AA13163 | Hs 54828 | Hs 54828 ESTs |
| 29500 | AA13164 | Hs 54829 | Hs 54829 ESTs |

WO 00/55633

PCT/US00/07044

FIGURE 3 (CONT.)

| | | | | |
|-------|---------|----------|-----|--|
| 20510 | 43513 | Hs 35100 | EST | |
| 20515 | 43514 | Hs 35100 | EST | |
| 20520 | 43515 | Hs 35100 | EST | |
| 20525 | 43516 | Hs 35100 | EST | |
| 20530 | 43517 | Hs 35100 | EST | |
| 20535 | 43518 | Hs 35100 | EST | |
| 20540 | 43519 | Hs 35100 | EST | |
| 20545 | 43520 | Hs 35100 | EST | |
| 20550 | 43521 | Hs 35100 | EST | |
| 20555 | 43522 | Hs 35100 | EST | |
| 20560 | 43523 | Hs 35100 | EST | |
| 20565 | 43524 | Hs 35100 | EST | |
| 20570 | 43525 | Hs 35100 | EST | |
| 20575 | 43526 | Hs 35100 | EST | |
| 20580 | 43527 | Hs 35100 | EST | |
| 20585 | 43528 | Hs 35100 | EST | |
| 20590 | 43529 | Hs 35100 | EST | |
| 20595 | 43530 | Hs 35100 | EST | |
| 20600 | 43531 | Hs 35100 | EST | |
| 20605 | 43532 | Hs 35100 | EST | |
| 20610 | 43533 | Hs 35100 | EST | |
| 20615 | 43534 | Hs 35100 | EST | |
| 20620 | 43535 | Hs 35100 | EST | |
| 20625 | 43536 | Hs 35100 | EST | |
| 20630 | 43537 | Hs 35100 | EST | |
| 20635 | 43538 | Hs 35100 | EST | |
| 20640 | 43539 | Hs 35100 | EST | |
| 20645 | 43540 | Hs 35100 | EST | |
| 20650 | 43541 | Hs 35100 | EST | |
| 20655 | 43542 | Hs 35100 | EST | |
| 20660 | 43543 | Hs 35100 | EST | |
| 20665 | 43544 | Hs 35100 | EST | |
| 20670 | 43545 | Hs 35100 | EST | |
| 20675 | 43546 | Hs 35100 | EST | |
| 20680 | 43547 | Hs 35100 | EST | |
| 20685 | 43548 | Hs 35100 | EST | |
| 20690 | 43549 | Hs 35100 | EST | |
| 20695 | 43550 | Hs 35100 | EST | |
| 20700 | 43551 | Hs 35100 | EST | |
| 20705 | 43552 | Hs 35100 | EST | |
| 20710 | 43553 | Hs 35100 | EST | |
| 20715 | 43554 | Hs 35100 | EST | |
| 20720 | 43555 | Hs 35100 | EST | |
| 20725 | 43556 | Hs 35100 | EST | |
| 20730 | 43557 | Hs 35100 | EST | |
| 20735 | 43558 | Hs 35100 | EST | |
| 20740 | 43559 | Hs 35100 | EST | |
| 20745 | 43560 | Hs 35100 | EST | |
| 20750 | 43561 | Hs 35100 | EST | |
| 20755 | 43562 | Hs 35100 | EST | |
| 20760 | 43563 | Hs 35100 | EST | |
| 20765 | 43564 | Hs 35100 | EST | |
| 20770 | 43565 | Hs 35100 | EST | |
| 20775 | 43566 | Hs 35100 | EST | |
| 20780 | 43567 | Hs 35100 | EST | |
| 20785 | 43568 | Hs 35100 | EST | |
| 20790 | 43569 | Hs 35100 | EST | |
| 20795 | 43570 | Hs 35100 | EST | |
| 20800 | 43571 | Hs 35100 | EST | |
| 20805 | 43572 | Hs 35100 | EST | |
| 20810 | 43573 | Hs 35100 | EST | |
| 20815 | 43574 | Hs 35100 | EST | |
| 20820 | 43575 | Hs 35100 | EST | |
| 20825 | 43576 | Hs 35100 | EST | |
| 20830 | 43577 | Hs 35100 | EST | |
| 20835 | 43578 | Hs 35100 | EST | |
| 20840 | 43579 | Hs 35100 | EST | |
| 20845 | 43580 | Hs 35100 | EST | |
| 20850 | 43581 | Hs 35100 | EST | |
| 20855 | 43582 | Hs 35100 | EST | |
| 20860 | 43583 | Hs 35100 | EST | |
| 20865 | 43584 | Hs 35100 | EST | |
| 20870 | 43585 | Hs 35100 | EST | |
| 20875 | 43586 | Hs 35100 | EST | |
| 20880 | 43587 | Hs 35100 | EST | |
| 20885 | 43588 | Hs 35100 | EST | |
| 20890 | 43589 | Hs 35100 | EST | |
| 20895 | 43590 | Hs 35100 | EST | |
| 20900 | 43591 | Hs 35100 | EST | |
| 20905 | 43592 | Hs 35100 | EST | |
| 20910 | 43593 | Hs 35100 | EST | |
| 20915 | 43594 | Hs 35100 | EST | |
| 20920 | 43595 | Hs 35100 | EST | |
| 20925 | 43596 | Hs 35100 | EST | |
| 20930 | 43597 | Hs 35100 | EST | |
| 20935 | 43598 | Hs 35100 | EST | |
| 20940 | 43599 | Hs 35100 | EST | |
| 20945 | 43600 | Hs 35100 | EST | |
| 20950 | 43601 | Hs 35100 | EST | |
| 20955 | 43602 | Hs 35100 | EST | |
| 20960 | 43603 | Hs 35100 | EST | |
| 20965 | 43604 | Hs 35100 | EST | |
| 20970 | 43605 | Hs 35100 | EST | |
| 20975 | 43606 | Hs 35100 | EST | |
| 20980 | 43607 | Hs 35100 | EST | |
| 20985 | 43608 | Hs 35100 | EST | |
| 20990 | 43609 | Hs 35100 | EST | |
| 20995 | 43610 | Hs 35100 | EST | |
| 21000 | 43611 | Hs 35100 | EST | |
| 21005 | 43612 | Hs 35100 | EST | |
| 21010 | 43613 | Hs 35100 | EST | |
| 21015 | 43614 | Hs 35100 | EST | |
| 21020 | 43615 | Hs 35100 | EST | |
| 21025 | 43616 | Hs 35100 | EST | |
| 21030 | 43617 | Hs 35100 | EST | |
| 21035 | 43618 | Hs 35100 | EST | |
| 21040 | 43619 | Hs 35100 | EST | |
| 21045 | 43620 | Hs 35100 | EST | |
| 21050 | 43621 | Hs 35100 | EST | |
| 21055 | 43622 | Hs 35100 | EST | |
| 21060 | 43623 | Hs 35100 | EST | |
| 21065 | 43624 | Hs 35100 | EST | |
| 21070 | 43625 | Hs 35100 | EST | |
| 21075 | 43626 | Hs 35100 | EST | |
| 21080 | 43627 | Hs 35100 | EST | |
| 21085 | 43628 | Hs 35100 | EST | |
| 21090 | 43629 | Hs 35100 | EST | |
| 21095 | 43630 | Hs 35100 | EST | |
| 21100 | 43631 | Hs 35100 | EST | |
| 21105 | 43632 | Hs 35100 | EST | |
| 21110 | 43633 | Hs 35100 | EST | |
| 21115 | 43634 | Hs 35100 | EST | |
| 21120 | 43635 | Hs 35100 | EST | |
| 21125 | 43636 | Hs 35100 | EST | |
| 21130 | 43637 | Hs 35100 | EST | |
| 21135 | 43638 | Hs 35100 | EST | |
| 21140 | 43639 | Hs 35100 | EST | |
| 21145 | 43640 | Hs 35100 | EST | |
| 21150 | 43641 | Hs 35100 | EST | |
| 21155 | 43642 | Hs 35100 | EST | |
| 21160 | 43643 | Hs 35100 | EST | |
| 21165 | 43644 | Hs 35100 | EST | |
| 21170 | 43645 | Hs 35100 | EST | |
| 21175 | 43646 | Hs 35100 | EST | |
| 21180 | 43647 | Hs 35100 | EST | |
| 21185 | 43648 | Hs 35100 | EST | |
| 21190 | 43649 | Hs 35100 | EST | |
| 21195 | 43650 | Hs 35100 | EST | |
| 21200 | 43651 | Hs 35100 | EST | |
| 21205 | 43652 | Hs 35100 | EST | |
| 21210 | 43653 | Hs 35100 | EST | |
| 21215 | 43654 | Hs 35100 | EST | |
| 21220 | 43655 | Hs 35100 | EST | |
| 21225 | 43656 | Hs 35100 | EST | |
| 21230 | 43657 | Hs 35100 | EST | |
| 21235 | 43658 | Hs 35100 | EST | |
| 21240 | 43659 | Hs 35100 | EST | |
| 21245 | 43660 | Hs 35100 | EST | |
| 21250 | 43661 | Hs 35100 | EST | |
| 21255 | 43662 | Hs 35100 | EST | |
| 21260 | 43663 | Hs 35100 | EST | |
| 21265 | 43664 | Hs 35100 | EST | |
| 21270 | 43665 | Hs 35100 | EST | |
| 21275 | 43666 | Hs 35100 | EST | |
| 21280 | 43667 | Hs 35100 | EST | |
| 21285 | 43668 | Hs 35100 | EST | |
| 21290 | 43669 | Hs 35100 | EST | |
| 21295 | 43670 | Hs 35100 | EST | |
| 21300 | 43671 | Hs 35100 | EST | |
| 21305 | 43672 | Hs 35100 | EST | |
| 21310 | 43673 | Hs 35100 | EST | |
| 21315 | 43674 | Hs 35100 | EST | |
| 21320 | 43675 | Hs 35100 | EST | |
| 21325 | 43676 | Hs 35100 | EST | |
| 21330 | 43677 | Hs 35100 | EST | |
| 21335 | 43678 | Hs 35100 | EST | |
| 21340 | 43679 | Hs 35100 | EST | |
| 21345 | 43680 | Hs 35100 | EST | |
| 21350 | 43681 | Hs 35100 | EST | |
| 21355 | 43682 | Hs 35100 | EST | |
| 21360 | 43683 | Hs 35100 | EST | |
| 21365 | 43684 | Hs 35100 | EST | |
| 21370 | 43685 | Hs 35100 | EST | |
| 21375 | 43686 | Hs 35100 | EST | |
| 21380 | 43687 | Hs 35100 | EST | |
| 21385 | 43688 | Hs 35100 | EST | |
| 21390 | 43689 | Hs 35100 | EST | |
| 21395 | 43690 | Hs 35100 | EST | |
| 21400 | 43691 | Hs 35100 | EST | |
| 21405 | 43692 | Hs 35100 | EST | |
| 21410 | 43693 | Hs 35100 | EST | |
| 21415 | 43694 | Hs 35100 | EST | |
| 21420 | 43695 | Hs 35100 | EST | |
| 21425 | 43696 | Hs 35100 | EST | |
| 21430 | 43697 | Hs 35100 | EST | |
| 21435 | 43698 | Hs 35100 | EST | |
| 21440 | 43699 | Hs 35100 | EST | |
| 21445 | 43700 | Hs 35100 | EST | |
| 21450 | 43701 | Hs 35100 | EST | |
| 21455 | 43702 | Hs 35100 | EST | |
| 21460 | 43703 | Hs 35100 | EST | |
| 21465 | 43704 | Hs 35100 | EST | |
| 21470 | 43705 | Hs 35100 | EST | |
| 21475 | 43706 | Hs 35100 | EST | |
| 21480 | 43707 | Hs 35100 | EST | |
| 21485 | 43708 | Hs 35100 | EST | |
| 21490 | 43709 | Hs 35100 | EST | |
| 21495 | 43710 | Hs 35100 | EST | |
| 21500 | 43711 | Hs 35100 | EST | |
| 21505 | 43712 | Hs 35100 | EST | |
| 21510 | 43713 | Hs 35100 | EST | |
| 21515 | 43714 | Hs 35100 | EST | |
| 21520 | 43715 | Hs 35100 | EST | |
| 21525 | 43716 | Hs 35100 | EST | |
| 21530 | 43717 | Hs 35100 | EST | |
| 21535 | 43718 | Hs 35100 | EST | |
| 21540 | 43719 | Hs 35100 | EST | |
| 21545 | 43720 | Hs 35100 | EST | |
| 21550 | 43721 | Hs 35100 | EST | |
| 21555 | 43722 | Hs 35100 | EST | |
| 21560 | 43723 | Hs 35100 | EST | |
| 21565 | 43724 | Hs 35100 | EST | |
| 21570 | 43725 | Hs 35100 | EST | |
| 21575 | 43726 | Hs 35100 | EST | |
| 21580 | 43727 | Hs 35100 | EST | |
| 21585 | 43728 | Hs 35100 | EST | |
| 21590 | 43729 | Hs 35100 | EST | |
| 21595 | 43730 | Hs 35100 | EST | |
| 21600 | 43731 | Hs 35100 | EST | |
| 21605 | 43732 | Hs 35100 | EST | |
| 21610 | 43733 | Hs 35100 | EST | |
| 21615 | 43734 | Hs 35100 | EST | |
| 21620 | 43735 | Hs 35100 | EST | |
| 21625 | 43736 | Hs 35100 | EST | |
| 21630 | 43737 | Hs 35100 | EST | |
| 21635 | 43738 | Hs 35100 | EST | |
| 21640 | 43739 | Hs 35100 | EST | |
| 21645 | 43740 | Hs 35100 | EST | |
| 21650 | 43741 | Hs 35100 | EST | |
| 21655 | 43742 | Hs 35100 | EST | |
| 21660 | 43743 | Hs 35100 | EST | |
| 21665 | 43744 | Hs 35100 | EST | |
| 21670 | 43745 | Hs 35100 | EST | |
| 21675 | 43746 | Hs 35100 | EST | |
| 21680 | 43747 | Hs 35100 | EST | |
| 21685 | 43748 | Hs 35100 | EST | |
| 21690 | 43749 | Hs 35100 | EST | |
| 21695 | 43750 | Hs 35100 | EST | |
| 21700 | 43751 | Hs 35100 | EST | |
| 21705 | 43752 | Hs 35100 | EST | |
| 21710 | 43753 | Hs 35100 | EST | |
| 21715 | 43754 | Hs 35100 | EST | |
| 21720 | 43755 | Hs 35100 | EST | |
| 21725 | 43756 | Hs 35100 | EST | |
| 21730 | 43757 | Hs 35100 | EST | |
| 21735 | 43758 | Hs 35100 | EST | |
| 21740 | 43759 | Hs 35100 | EST | |
| 21745 | 43760 | Hs 35100 | EST | |
| 21750 | 43761 | Hs 35100 | EST | |
| 21755 | 43762 | Hs 35100 | EST | |
| 21760 | 43763 | Hs 35100 | EST | |
| 21765 | 43764 | Hs 35100 | EST | |
| 21770 | 43765</ | | | |

20/236

| | | | | |
|----|---|--------------|--------------------|--|
| 1 | 3 | NS5058 | Hs 0706 E57a | |
| 2 | 3 | AA33209 | Hs 0706 E57a | |
| 3 | 3 | NS5059 | Hs 0706 E57a | |
| 4 | 3 | NS1164 | Hs 0351 E57a | |
| 5 | 3 | NS1165 | Hs 0351 E57a | |
| 6 | 3 | Q24646-PT233 | ES1 - NS2646-PT233 | |
| 7 | 3 | NS5060 | Hs 0706 E57a | |
| 8 | 3 | NS5061 | Hs 0706 E57a | |
| 9 | 3 | NS5062 | Hs 0706 E57a | |
| 10 | 3 | NS5063 | Hs 0706 E57a | |
| 11 | 3 | NS5064 | Hs 0706 E57a | |
| 12 | 3 | NS5065 | Hs 0706 E57a | |
| 13 | 3 | NS5066 | Hs 0706 E57a | |
| 14 | 3 | NS5067 | Hs 0706 E57a | |
| 15 | 3 | NS5068 | Hs 0706 E57a | |
| 16 | 3 | NS5069 | Hs 0706 E57a | |
| 17 | 3 | NS5070 | Hs 0706 E57a | |
| 18 | 3 | NS5071 | Hs 0706 E57a | |
| 19 | 3 | NS5072 | Hs 0706 E57a | |
| 20 | 3 | NS5073 | Hs 0706 E57a | |
| 21 | 3 | NS5074 | Hs 0706 E57a | |
| 22 | 3 | NS5075 | Hs 0706 E57a | |
| 23 | 3 | NS5076 | Hs 0706 E57a | |
| 24 | 3 | NS5077 | Hs 0706 E57a | |
| 25 | 3 | NS5078 | Hs 0706 E57a | |
| 26 | 3 | NS5079 | Hs 0706 E57a | |
| 27 | 3 | NS5080 | Hs 0706 E57a | |
| 28 | 3 | NS5081 | Hs 0706 E57a | |
| 29 | 3 | NS5082 | Hs 0706 E57a | |
| 30 | 3 | NS5083 | Hs 0706 E57a | |
| 31 | 3 | NS5084 | Hs 0706 E57a | |
| 32 | 3 | NS5085 | Hs 0706 E57a | |
| 33 | 3 | NS5086 | Hs 0706 E57a | |
| 34 | 3 | NS5087 | Hs 0706 E57a | |
| 35 | 3 | NS5088 | Hs 0706 E57a | |
| 36 | 3 | NS5089 | Hs 0706 E57a | |
| 37 | 3 | NS5090 | Hs 0706 E57a | |
| 38 | 3 | NS5091 | Hs 0706 E57a | |
| 39 | 3 | NS5092 | Hs 0706 E57a | |
| 40 | 3 | NS5093 | Hs 0706 E57a | |
| 41 | 3 | NS5094 | Hs 0706 E57a | |
| 42 | 3 | NS5095 | Hs 0706 E57a | |
| 43 | 3 | NS5096 | Hs 0706 E57a | |
| 44 | 3 | NS5097 | Hs 0706 E57a | |
| 45 | 3 | NS5098 | Hs 0706 E57a | |
| 46 | 3 | NS5099 | Hs 0706 E57a | |
| 47 | 3 | NS5100 | Hs 0706 E57a | |
| 48 | 3 | NS5101 | Hs 0706 E57a | |
| 49 | 3 | NS5102 | Hs 0706 E57a | |
| 50 | 3 | NS5103 | Hs 0706 E57a | |
| 51 | 3 | NS5104 | Hs 0706 E57a | |
| 52 | 3 | NS5105 | Hs 0706 E57a | |
| 53 | 3 | NS5106 | Hs 0706 E57a | |
| 54 | 3 | NS5107 | Hs 0706 E57a | |
| 55 | 3 | NS5108 | Hs 0706 E57a | |
| 56 | 3 | NS5109 | Hs 0706 E57a | |
| 57 | 3 | NS5110 | Hs 0706 E57a | |
| 58 | 3 | NS5111 | Hs 0706 E57a | |
| 59 | 3 | NS5112 | Hs 0706 E57a | |
| 60 | 3 | NS5113 | Hs 0706 E57a | |
| 61 | 3 | NS5114 | Hs 0706 E57a | |
| 62 | 3 | NS5115 | Hs 0706 E57a | |
| 63 | 3 | NS5116 | Hs 0706 E57a | |
| 64 | 3 | NS5117 | Hs 0706 E57a | |
| 65 | 3 | NS5118 | Hs 0706 E57a | |
| 66 | 3 | NS5119 | Hs 0706 E57a | |
| 67 | 3 | NS5120 | Hs 0706 E57a | |
| 68 | 3 | NS5121 | Hs 0706 E57a | |
| 69 | 3 | NS5122 | Hs 0706 E57a | |
| 70 | 3 | NS5123 | Hs 0706 E57a | |
| 71 | 3 | NS5124 | Hs 0706 E57a | |
| 72 | 3 | NS5125 | Hs 0706 E57a | |
| 73 | 3 | NS5126 | Hs 0706 E57a | |
| 74 | 3 | NS5127 | Hs 0706 E57a | |
| 75 | 3 | NS5128 | Hs 0706 E57a | |
| 76 | 3 | NS5129 | Hs 0706 E57a | |
| 77 | 3 | NS5130 | Hs 0706 E57a | |
| 78 | 3 | NS5131 | Hs 0706 E57a | |
| 79 | 3 | NS5132 | Hs 0706 E57a | |
| 80 | 3 | NS5133 | Hs 0706 E57a | |
| 81 | 3 | NS5134 | Hs 0706 E57a | |
| 82 | 3 | NS5135 | Hs 0706 E57a | |
| 83 | 3 | NS5136 | Hs 0706 E57a | |
| 84 | 3 | NS5137 | Hs 0706 E57a | |
| 85 | 3 | NS5138 | Hs 0706 E57a | |
| 86 | | | | |

FIGURE 3 (CONT.)

| | | | | |
|-------|--------|----------------|-----|------------------|
| 2447 | 235108 | Hs 27382 | EST | |
| 1 | 4 | Hs 42221 | EST | Hs 42221 |
| 1195 | 4 | Ga 157-H1-4247 | EST | Hs 42415 H1-4247 |
| 1196 | 4 | G3884-H12-127 | EST | Hs 42415 H12-127 |
| 34027 | 4 | Hs 40233 | EST | Hs 40233 |
| 34028 | 4 | Hs 40235 | EST | Hs 40235 |
| 34029 | 4 | Hs 40237 | EST | Hs 40237 |
| 11365 | 4 | Hs 38504 | EST | Hs 38504 |
| 8225 | 4 | Hs 32576 | EST | Hs 32576 |
| 8226 | 4 | Hs 32578 | EST | Hs 32578 |
| 34781 | 4 | Hs 125014 | EST | Hs 125014 |
| 34782 | 4 | Hs 125015 | EST | Hs 125015 |
| 34783 | 4 | Hs 125016 | EST | Hs 125016 |
| 34784 | 4 | Hs 125017 | EST | Hs 125017 |
| 34785 | 4 | Hs 125018 | EST | Hs 125018 |
| 11566 | 4 | Hs 125019 | EST | Hs 125019 |
| 38822 | 4 | Hs 11582 | EST | Hs 11582 |
| 38823 | 4 | Hs 11583 | EST | Hs 11583 |
| 38824 | 4 | Hs 11584 | EST | Hs 11584 |
| 38825 | 4 | Hs 11585 | EST | Hs 11585 |
| 38826 | 4 | Hs 11586 | EST | Hs 11586 |
| 38827 | 4 | Hs 11587 | EST | Hs 11587 |
| 38828 | 4 | Hs 11588 | EST | Hs 11588 |
| 38829 | 4 | Hs 11589 | EST | Hs 11589 |
| 38830 | 4 | Hs 11590 | EST | Hs 11590 |
| 38831 | 4 | Hs 11591 | EST | Hs 11591 |
| 38832 | 4 | Hs 11592 | EST | Hs 11592 |
| 38833 | 4 | Hs 11593 | EST | Hs 11593 |
| 38834 | 4 | Hs 11594 | EST | Hs 11594 |
| 38835 | 4 | Hs 11595 | EST | Hs 11595 |
| 38836 | 4 | Hs 11596 | EST | Hs 11596 |
| 38837 | 4 | Hs 11597 | EST | Hs 11597 |
| 38838 | 4 | Hs 11598 | EST | Hs 11598 |
| 38839 | 4 | Hs 11599 | EST | Hs 11599 |
| 38840 | 4 | Hs 11600 | EST | Hs 11600 |
| 38841 | 4 | Hs 11601 | EST | Hs 11601 |
| 38842 | 4 | Hs 11602 | EST | Hs 11602 |
| 38843 | 4 | Hs 11603 | EST | Hs 11603 |
| 38844 | 4 | Hs 11604 | EST | Hs 11604 |
| 38845 | 4 | Hs 11605 | EST | Hs 11605 |
| 38846 | 4 | Hs 11606 | EST | Hs 11606 |
| 38847 | 4 | Hs 11607 | EST | Hs 11607 |
| 38848 | 4 | Hs 11608 | EST | Hs 11608 |
| 38849 | 4 | Hs 11609 | EST | Hs 11609 |
| 38850 | 4 | Hs 11610 | EST | Hs 11610 |
| 38851 | 4 | Hs 11611 | EST | Hs 11611 |
| 38852 | 4 | Hs 11612 | EST | Hs 11612 |
| 38853 | 4 | Hs 11613 | EST | Hs 11613 |
| 38854 | 4 | Hs 11614 | EST | Hs 11614 |
| 38855 | 4 | Hs 11615 | EST | Hs 11615 |
| 38856 | 4 | Hs 11616 | EST | Hs 11616 |
| 38857 | 4 | Hs 11617 | EST | Hs 11617 |
| 38858 | 4 | Hs 11618 | EST | Hs 11618 |
| 38859 | 4 | Hs 11619 | EST | Hs 11619 |
| 38860 | 4 | Hs 11620 | EST | Hs 11620 |
| 38861 | 4 | Hs 11621 | EST | Hs 11621 |
| 38862 | 4 | Hs 11622 | EST | Hs 11622 |
| 38863 | 4 | Hs 11623 | EST | Hs 11623 |
| 38864 | 4 | Hs 11624 | EST | Hs 11624 |
| 38865 | 4 | Hs 11625 | EST | Hs 11625 |
| 38866 | 4 | Hs 11626 | EST | Hs 11626 |
| 38867 | 4 | Hs 11627 | EST | Hs 11627 |
| 38868 | 4 | Hs 11628 | EST | Hs 11628 |
| 38869 | 4 | Hs 11629 | EST | Hs 11629 |
| 38870 | 4 | Hs 11630 | EST | Hs 11630 |
| 38871 | 4 | Hs 11631 | EST | Hs 11631 |
| 38872 | 4 | Hs 11632 | EST | Hs 11632 |
| 38873 | 4 | Hs 11633 | EST | Hs 11633 |
| 38874 | 4 | Hs 11634 | EST | Hs 11634 |
| 38875 | 4 | Hs 11635 | EST | Hs 11635 |
| 38876 | 4 | Hs 11636 | EST | Hs 11636 |
| 38877 | 4 | Hs 11637 | EST | Hs 11637 |
| 38878 | 4 | Hs 11638 | EST | Hs 11638 |
| 38879 | 4 | Hs 11639 | EST | Hs 11639 |
| 38880 | 4 | Hs 11640 | EST | Hs 11640 |
| 38881 | 4 | Hs 11641 | EST | Hs 11641 |
| 38882 | 4 | Hs 11642 | EST | Hs 11642 |
| 38883 | 4 | Hs 11643 | EST | Hs 11643 |
| 38884 | 4 | Hs 11644 | EST | Hs 11644 |
| 38885 | 4 | Hs 11645 | EST | Hs 11645 |
| 38886 | 4 | Hs 11646 | EST | Hs 11646 |
| 38887 | 4 | Hs 11647 | EST | Hs 11647 |
| 38888 | 4 | Hs 11648 | EST | Hs 11648 |
| 38889 | 4 | Hs 11649 | EST | Hs 11649 |
| 38890 | 4 | Hs 11650 | EST | Hs 11650 |
| 38891 | 4 | Hs 11651 | EST | Hs 11651 |
| 38892 | 4 | Hs 11652 | EST | Hs 11652 |
| 38893 | 4 | Hs 11653 | EST | Hs 11653 |
| 38894 | 4 | Hs 11654 | EST | Hs 11654 |
| 38895 | 4 | Hs 11655 | EST | Hs 11655 |
| 38896 | 4 | Hs 11656 | EST | Hs 11656 |
| 38897 | 4 | Hs 11657 | EST | Hs 11657 |
| 38898 | 4 | Hs 11658 | EST | Hs 11658 |
| 38899 | 4 | Hs 11659 | EST | Hs 11659 |
| 38900 | 4 | Hs 11660 | EST | Hs 11660 |
| 38901 | 4 | Hs 11661 | EST | Hs 11661 |
| 38902 | 4 | Hs 11662 | EST | Hs 11662 |
| 38903 | 4 | Hs 11663 | EST | Hs 11663 |
| 38904 | 4 | Hs 11664 | EST | Hs 11664 |
| 38905 | 4 | Hs 11665 | EST | Hs 11665 |
| 38906 | 4 | Hs 11666 | EST | Hs 11666 |
| 38907 | 4 | Hs 11667 | EST | Hs 11667 |
| 38908 | 4 | Hs 11668 | EST | Hs 11668 |
| 38909 | 4 | Hs 11669 | EST | Hs 11669 |
| 38910 | 4 | Hs 11670 | EST | Hs 11670 |
| 38911 | 4 | Hs 11671 | EST | Hs 11671 |
| 38912 | 4 | Hs 11672 | EST | Hs 11672 |
| 38913 | 4 | Hs 11673 | EST | Hs 11673 |
| 38914 | 4 | Hs 11674 | EST | Hs 11674 |
| 38915 | 4 | Hs 11675 | EST | Hs 11675 |
| 38916 | 4 | Hs 11676 | EST | Hs 11676 |
| 38917 | 4 | Hs 11677 | EST | Hs 11677 |
| 38918 | 4 | Hs 11678 | EST | Hs 11678 |
| 38919 | 4 | Hs 11679 | EST | Hs 11679 |
| 38920 | 4 | Hs 11680 | EST | Hs 11680 |
| 38921 | 4 | Hs 11681 | EST | Hs 11681 |
| 38922 | 4 | Hs 11682 | EST | Hs 11682 |
| 38923 | 4 | Hs 11683 | EST | Hs 11683 |
| 38924 | 4 | Hs 11684 | EST | Hs 11684 |
| 38925 | 4 | Hs 11685 | EST | Hs 11685 |
| 38926 | 4 | Hs 11686 | EST | Hs 11686 |
| 38927 | 4 | Hs 11687 | EST | Hs 11687 |
| 38928 | 4 | Hs 11688 | EST | Hs 11688 |
| 38929 | 4 | Hs 11689 | EST | Hs 11689 |
| 38930 | 4 | Hs 11690 | EST | Hs 11690 |
| 38931 | 4 | Hs 11691 | EST | Hs 11691 |
| 38932 | 4 | Hs 11692 | EST | Hs 11692 |
| 38933 | 4 | Hs 11693 | EST | Hs 11693 |
| 38934 | 4 | Hs 11694 | EST | Hs 11694 |
| 38935 | 4 | Hs 11695 | EST | Hs 11695 |
| 38936 | 4 | Hs 11696 | EST | Hs 11696 |
| 38937 | 4 | Hs 11697 | EST | Hs 11697 |
| 38938 | 4 | Hs 11698 | EST | Hs 11698 |
| 38939 | 4 | Hs 11699 | EST | Hs 11699 |
| 38940 | 4 | Hs 11700 | EST | Hs 11700 |
| 38941 | 4 | Hs 11701 | EST | Hs 11701 |
| 38942 | 4 | Hs 11702 | EST | Hs 11702 |
| 38943 | 4 | Hs 11703 | EST | Hs 11703 |
| 38944 | 4 | Hs 11704 | EST | Hs 11704 |
| 38945 | 4 | Hs 11705 | EST | Hs 11705 |
| 38946 | 4 | Hs 11706 | EST | Hs 11706 |
| 38947 | 4 | Hs 11707 | EST | Hs 11707 |
| 38948 | 4 | Hs 11708 | EST | Hs 11708 |
| 38949 | 4 | Hs 11709 | EST | Hs 11709 |
| 38950 | 4 | Hs 11710 | EST | Hs 11710 |
| 38951 | 4 | Hs 11711 | EST | Hs 11711 |
| 38952 | 4 | Hs 11712 | EST | Hs 11712 |
| 38953 | 4 | Hs 11713 | EST | Hs 11713 |
| 38954 | 4 | Hs 11714 | EST | Hs 11714 |
| 38955 | 4 | Hs 11715 | EST | Hs 11715 |
| 38956 | 4 | Hs 11716 | EST | Hs 11716 |
| 38957 | 4 | Hs 11717 | EST | Hs 11717 |
| 38958 | 4 | Hs 11718 | EST | Hs 11718 |
| 38959 | 4 | Hs 11719 | EST | Hs 11719 |
| 38960 | 4 | Hs 11720 | EST | Hs 11720 |
| 38961 | 4 | Hs 11721 | EST | Hs 11721 |
| 38962 | 4 | Hs 11722 | EST | Hs 11722 |
| 38963 | 4 | Hs 11723 | EST | Hs 11723 |
| 38964 | 4 | Hs 11724 | EST | Hs 11724 |
| 38965 | 4 | Hs 11725 | EST | Hs 11725 |
| 38966 | 4 | Hs 11726 | EST | Hs 11726 |
| 38967 | 4 | Hs 11727 | EST | Hs 11727 |
| 38968 | 4 | Hs 11728 | EST | Hs 11728 |
| 38969 | 4 | Hs 11729 | EST | Hs 11729 |
| 38970 | 4 | Hs 11730 | EST | Hs 11730 |
| 38971 | 4 | Hs 11731 | EST | Hs 11731 |
| 38972 | 4 | Hs 11732 | EST | Hs 11732 |
| 38973 | 4 | Hs 11733 | EST | Hs 11733 |
| 38974 | 4 | Hs 11734 | EST | Hs 11734 |
| 38975 | 4 | Hs 11735 | EST | Hs 11735 |
| 38976 | 4 | Hs 11736 | EST | Hs 11736 |
| 38977 | 4 | Hs 11737 | EST | Hs 11737 |
| 38978 | 4 | Hs 11738 | EST | Hs 11738 |
| 38979 | 4 | Hs 11739 | EST | Hs 11739 |
| 38980 | 4 | Hs 11740 | EST | Hs 11740 |
| 38981 | 4 | Hs 11741 | EST | Hs 11741 |
| 38982 | 4 | Hs 11742 | EST | Hs 11742 |
| 38983 | 4 | Hs 11743 | EST | Hs 11743 |
| 38984 | 4 | Hs 11744 | EST | Hs 11744 |
| 38985 | 4 | Hs 11745 | EST | Hs 11745 |
| 38986 | 4 | Hs 11746 | EST | Hs 11746 |
| 38987 | 4 | Hs 11747 | EST | Hs 11747 |
| 38988 | 4 | Hs 11748 | EST | Hs 11748 |
| 38989 | 4 | Hs 11749 | EST | Hs 11749 |
| 38990 | 4 | Hs 11750 | EST | Hs 11750 |
| 38991 | 4 | Hs 11751 | EST | Hs 11751 |
| 38992 | 4 | Hs 11752 | EST | Hs 11752 |
| 38993 | 4 | Hs 11753 | EST | Hs 11753 |
| 38994 | 4 | Hs 11754 | EST | Hs 11754 |
| 38995 | 4 | Hs 11755 | EST | Hs 11755 |
| 38996 | 4 | Hs 11756 | EST | Hs 11756 |
| 38997 | 4 | Hs 11757 | EST | Hs 11757 |
| 38998 | 4 | Hs 11758 | EST | Hs 11758 |
| 38999 | 4 | Hs 11759 | EST | Hs 11759 |
| 39000 | 4 | Hs 11760 | EST | Hs 11760 |

FIGURE 3 (CONT.)

[illegible]

PCT/US00/07044

23/236

5

FIGURE 3 (CONT.)

[illegible]

PCT/US00/07044

FIGURE 3 (CONT.)

[illegible]

26/236

29/236

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WO 00/55633

PCT/US00/07044

FIGURE 3 (CONT.)

| | | | | | |
|------|-----|----------|----------|------|--|
| 9556 | 24 | HA181437 | HA132031 | ESTs | |
| 9557 | 25 | HA181438 | HA132032 | ESTs | |
| 9558 | 26 | HA181439 | HA132033 | ESTs | |
| 9559 | 27 | HA181440 | HA132034 | ESTs | |
| 9560 | 28 | HA181441 | HA132035 | ESTs | |
| 9561 | 29 | HA181442 | HA132036 | ESTs | |
| 9562 | 30 | HA181443 | HA132037 | ESTs | |
| 9563 | 31 | HA181444 | HA132038 | ESTs | |
| 9564 | 32 | HA181445 | HA132039 | ESTs | |
| 9565 | 33 | HA181446 | HA132040 | ESTs | |
| 9566 | 34 | HA181447 | HA132041 | ESTs | |
| 9567 | 35 | HA181448 | HA132042 | ESTs | |
| 9568 | 36 | HA181449 | HA132043 | ESTs | |
| 9569 | 37 | HA181450 | HA132044 | ESTs | |
| 9570 | 38 | HA181451 | HA132045 | ESTs | |
| 9571 | 39 | HA181452 | HA132046 | ESTs | |
| 9572 | 40 | HA181453 | HA132047 | ESTs | |
| 9573 | 41 | HA181454 | HA132048 | ESTs | |
| 9574 | 42 | HA181455 | HA132049 | ESTs | |
| 9575 | 43 | HA181456 | HA132050 | ESTs | |
| 9576 | 44 | HA181457 | HA132051 | ESTs | |
| 9577 | 45 | HA181458 | HA132052 | ESTs | |
| 9578 | 46 | HA181459 | HA132053 | ESTs | |
| 9579 | 47 | HA181460 | HA132054 | ESTs | |
| 9580 | 48 | HA181461 | HA132055 | ESTs | |
| 9581 | 49 | HA181462 | HA132056 | ESTs | |
| 9582 | 50 | HA181463 | HA132057 | ESTs | |
| 9583 | 51 | HA181464 | HA132058 | ESTs | |
| 9584 | 52 | HA181465 | HA132059 | ESTs | |
| 9585 | 53 | HA181466 | HA132060 | ESTs | |
| 9586 | 54 | HA181467 | HA132061 | ESTs | |
| 9587 | 55 | HA181468 | HA132062 | ESTs | |
| 9588 | 56 | HA181469 | HA132063 | ESTs | |
| 9589 | 57 | HA181470 | HA132064 | ESTs | |
| 9590 | 58 | HA181471 | HA132065 | ESTs | |
| 9591 | 59 | HA181472 | HA132066 | ESTs | |
| 9592 | 60 | HA181473 | HA132067 | ESTs | |
| 9593 | 61 | HA181474 | HA132068 | ESTs | |
| 9594 | 62 | HA181475 | HA132069 | ESTs | |
| 9595 | 63 | HA181476 | HA132070 | ESTs | |
| 9596 | 64 | HA181477 | HA132071 | ESTs | |
| 9597 | 65 | HA181478 | HA132072 | ESTs | |
| 9598 | 66 | HA181479 | HA132073 | ESTs | |
| 9599 | 67 | HA181480 | HA132074 | ESTs | |
| 9600 | 68 | HA181481 | HA132075 | ESTs | |
| 9601 | 69 | HA181482 | HA132076 | ESTs | |
| 9602 | 70 | HA181483 | HA132077 | ESTs | |
| 9603 | 71 | HA181484 | HA132078 | ESTs | |
| 9604 | 72 | HA181485 | HA132079 | ESTs | |
| 9605 | 73 | HA181486 | HA132080 | ESTs | |
| 9606 | 74 | HA181487 | HA132081 | ESTs | |
| 9607 | 75 | HA181488 | HA132082 | ESTs | |
| 9608 | 76 | HA181489 | HA132083 | ESTs | |
| 9609 | 77 | HA181490 | HA132084 | ESTs | |
| 9610 | 78 | HA181491 | HA132085 | ESTs | |
| 9611 | 79 | HA181492 | HA132086 | ESTs | |
| 9612 | 80 | HA181493 | HA132087 | ESTs | |
| 9613 | 81 | HA181494 | HA132088 | ESTs | |
| 9614 | 82 | HA181495 | HA132089 | ESTs | |
| 9615 | 83 | HA181496 | HA132090 | ESTs | |
| 9616 | 84 | HA181497 | HA132091 | ESTs | |
| 9617 | 85 | HA181498 | HA132092 | ESTs | |
| 9618 | 86 | HA181499 | HA132093 | ESTs | |
| 9619 | 87 | HA181500 | HA132094 | ESTs | |
| 9620 | 88 | HA181501 | HA132095 | ESTs | |
| 9621 | 89 | HA181502 | HA132096 | ESTs | |
| 9622 | 90 | HA181503 | HA132097 | ESTs | |
| 9623 | 91 | HA181504 | HA132098 | ESTs | |
| 9624 | 92 | HA181505 | HA132099 | ESTs | |
| 9625 | 93 | HA181506 | HA132100 | ESTs | |
| 9626 | 94 | HA181507 | HA132101 | ESTs | |
| 9627 | 95 | HA181508 | HA132102 | ESTs | |
| 9628 | 96 | HA181509 | HA132103 | ESTs | |
| 9629 | 97 | HA181510 | HA132104 | ESTs | |
| 9630 | 98 | HA181511 | HA132105 | ESTs | |
| 9631 | 99 | HA181512 | HA132106 | ESTs | |
| 9632 | 100 | HA181513 | HA132107 | ESTs | |
| 9633 | 101 | HA181514 | HA132108 | ESTs | |
| 9634 | 102 | HA181515 | HA132109 | ESTs | |
| 9635 | 103 | HA181516 | HA132110 | ESTs | |
| 9636 | 104 | HA181517 | HA132111 | ESTs | |
| 9637 | 105 | HA181518 | HA132112 | ESTs | |
| 9638 | 106 | HA181519 | HA132113 | ESTs | |
| 9639 | 107 | HA181520 | HA132114 | ESTs | |
| 9640 | 108 | HA181521 | HA132115 | ESTs | |
| 9641 | 109 | HA181522 | HA132116 | ESTs | |
| 9642 | 110 | HA181523 | HA132117 | ESTs | |
| 9643 | 111 | HA181524 | HA132118 | ESTs | |
| 9644 | 112 | HA181525 | HA132119 | ESTs | |
| 9645 | 113 | HA181526 | HA132120 | ESTs | |
| 9646 | 114 | HA181527 | HA132121 | ESTs | |
| 9647 | 115 | HA181528 | HA132122 | ESTs | |
| 9648 | 116 | HA181529 | HA132123 | ESTs | |
| 9649 | 117 | HA181530 | HA132124 | ESTs | |
| 9650 | 118 | HA181531 | HA132125 | ESTs | |
| 9651 | 119 | HA181532 | HA132126 | ESTs | |
| 9652 | 120 | HA181533 | HA132127 | ESTs | |
| 9653 | 121 | HA181534 | HA132128 | ESTs | |
| 9654 | 122 | HA181535 | HA132129 | ESTs | |
| 9655 | 123 | HA181536 | HA132130 | ESTs | |
| 9656 | 124 | HA181537 | HA132131 | ESTs | |
| 9657 | 125 | HA181538 | HA132132 | ESTs | |
| 9658 | 126 | HA181539 | HA132133 | ESTs | |
| 9659 | 127 | HA181540 | HA132134 | ESTs | |
| 9660 | 128 | HA181541 | HA132135 | ESTs | |
| 9661 | 129 | HA181542 | HA132136 | ESTs | |
| 9662 | 130 | HA181543 | HA132137 | ESTs | |
| 9663 | 131 | HA181544 | HA132138 | ESTs | |
| 9664 | 132 | HA181545 | HA132139 | ESTs | |
| 9665 | 133 | HA181546 | HA132140 | ESTs | |
| 9666 | 134 | HA181547 | HA132141 | ESTs | |
| 9667 | 135 | HA181548 | HA132142 | ESTs | |
| 9668 | 136 | HA181549 | HA132143 | ESTs | |
| 9669 | 137 | HA181550 | HA132144 | ESTs | |
| 9670 | 138 | HA181551 | HA132145 | ESTs | |
| 9671 | 139 | HA181552 | HA132146 | ESTs | |
| 9672 | 140 | HA181553 | HA132147 | ESTs | |
| 9673 | 141 | HA181554 | HA132148 | ESTs | |
| 9674 | 142 | HA181555 | HA132149 | ESTs | |
| 9675 | 143 | HA181556 | HA132150 | ESTs | |
| 9676 | 144 | HA181557 | HA132151 | ESTs | |
| 9677 | 145 | HA181558 | HA132152 | ESTs | |
| 9678 | 146 | HA181559 | HA132153 | ESTs | |
| 9679 | 147 | HA181560 | HA132154 | ESTs | |
| 9680 | 148 | HA181561 | HA132155 | ESTs | |
| 9681 | 149 | HA181562 | HA132156 | ESTs | |
| 9682 | 150 | HA181563 | HA132157 | ESTs | |
| 9683 | 151 | HA181564 | HA132158 | ESTs | |
| 9684 | 152 | HA181565 | HA132159 | ESTs | |
| 9685 | 153 | HA181566 | HA132160 | ESTs | |
| 9686 | 154 | HA181567 | HA132161 | ESTs | |
| 9687 | 155 | HA181568 | HA132162 | ESTs | |
| 9688 | 156 | HA181569 | HA132163 | ESTs | |
| 9689 | 157 | HA181570 | HA132164 | ESTs | |
| 9690 | 158 | HA181571 | HA132165 | ESTs | |
| 9691 | 159 | HA181572 | HA132166 | ESTs | |
| 9692 | 160 | HA181573 | HA132167 | ESTs | |
| 9693 | 161 | HA181574 | HA132168 | ESTs | |
| 9694 | 162 | HA181575 | HA132169 | ESTs | |
| 9695 | 163 | HA181576 | HA132170 | ESTs | |
| 9696 | 164 | HA181577 | HA132171 | ESTs | |
| 9697 | 165 | HA181578 | HA132172 | ESTs | |
| 9698 | 166 | HA181579 | HA132173 | ESTs | |
| 9699 | 167 | HA181580 | HA132174 | ESTs | |
| 9700 | 168 | HA181581 | HA132175 | ESTs | |
| 9701 | 169 | HA181582 | HA132176 | ESTs | |
| 9702 | 170 | HA181583 | HA132177 | ESTs | |
| 9703 | 171 | HA181584 | HA132178 | ESTs | |
| 9704 | 172 | HA181585 | HA132179 | ESTs | |
| 9705 | 173 | HA181586 | HA132180 | ESTs | |
| 9706 | 174 | HA181587 | HA132181 | ESTs | |
| 9707 | 175 | HA181588 | HA132182 | ESTs | |
| 9708 | 176 | HA181589 | HA132183 | ESTs | |
| 9709 | 177 | HA181590 | HA132184 | ESTs | |
| 9710 | 178 | HA181591 | HA132185 | ESTs | |
| 9711 | 179 | HA181592 | HA132186 | ESTs | |
| 9712 | 180 | HA181593 | HA132187 | ESTs | |
| 9713 | 181 | HA181594 | HA132188 | ESTs | |
| 9714 | 182 | HA181595 | HA132189 | ESTs | |
| 9715 | 183 | HA181596 | HA132190 | ESTs | |
| 9716 | 184 | HA181597 | HA132191 | ESTs | |
| 9717 | 185 | HA181598 | HA132192 | ESTs | |
| 9718 | 186 | HA181599 | HA132193 | ESTs | |
| 9719 | 187 | HA181600 | HA132194 | ESTs | |
| 9720 | 188 | HA181601 | HA132195 | ESTs | |
| 9721 | 189 | HA181602 | HA132196 | ESTs | |
| 9722 | 190 | HA181603 | HA132197 | ESTs | |
| 9723 | 191 | HA181604 | HA132198 | ESTs | |
| 9724 | 192 | HA181605 | HA132199 | ESTs | |
| 9725 | 193 | HA181606 | HA132200 | ESTs | |
| 9726 | 194 | HA181607 | HA132201 | ESTs | |
| 9727 | 195 | HA181608 | HA132202 | ESTs | |
| 9728 | 196 | HA181609 | HA132203 | ESTs | |
| 9729 | 197 | HA181610 | HA132204 | ESTs | |
| 9730 | 198 | HA181611 | HA132205 | ESTs | |
| 9731 | 199 | HA181612 | HA132206 | ESTs | |
| 9732 | 200 | HA181613 | HA132207 | ESTs | |
| 9733 | 201 | HA181614 | HA132208 | ESTs | |
| 9734 | 202 | HA181615 | HA132209 | ESTs | |
| 9735 | 203 | HA181616 | HA132210 | ESTs | |
| 9736 | 204 | HA181617 | HA132211 | ESTs | |
| 9737 | 205 | HA181618 | HA132212 | ESTs | |
| 9738 | 206 | HA181619 | HA132213 | ESTs | |
| 9739 | 207 | HA181620 | HA132214 | ESTs | |
| 9740 | 208 | HA181621 | HA132215 | ESTs | |
| 9741 | 209 | HA181622 | HA132216 | ESTs | |
| 9742 | 210 | HA181623 | HA132217 | ESTs | |
| 9743 | 211 | HA181624 | HA132218 | ESTs | |
| 9744 | 212 | HA181625 | HA132219 | ESTs | |
| 9745 | 213 | HA181626 | HA132220 | ESTs | |
| 9746 | 214 | HA181627 | HA132221 | ESTs | |
| 9747 | 215 | HA181628 | HA132222 | ESTs | |
| 9748 | 216 | HA181629 | HA132223 | ESTs | |
| 9749 | 217 | HA181630 | HA132224 | ESTs | |
| 9750 | 218 | HA181631 | HA132225 | ESTs | |
| 9751 | 219 | HA181632 | HA132226 | ESTs | |
| 9752 | 220 | HA181633 | HA132227 | ESTs | |
| 9753 | 221 | HA181634 | HA132228 | ESTs | |
| 9754 | 222 | HA181635 | HA132229 | ESTs | |
| 9755 | 223 | HA181636 | HA132230 | ESTs | |
| 9756 | 224 | HA181637 | HA132231 | ESTs | |
| 9757 | 225 | HA181638 | HA132232 | ESTs | |
| 9758 | 226 | HA181639 | HA132233 | ESTs | |
| 9759 | 227 | HA181640 | HA132234 | ESTs | |
| 9760 | 228 | HA181641 | HA132235 | ESTs | |
| 9761 | 229 | HA181642 | HA132236 | ESTs | |
| 9762 | 230 | HA181643 | HA132237 | ESTs | |
| 9763 | 231 | HA181644 | HA132238 | ESTs | |
| 9764 | 232 | HA181645 | HA132239 | ESTs | |
| 9765 | 233 | HA181646 | HA132240 | ESTs | |
| 9766 | | | | | |

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FIGURE 3 (CONT.)

| | | | | | |
|-------|----|----------|----------|------|--|
| 12552 | 23 | AA454542 | Hs 29511 | ESTs | |
| 12553 | 23 | AA454543 | Hs 29511 | ESTs | |
| 20001 | 23 | AA454544 | Hs 29511 | ESTs | |
| 21434 | 23 | AA454545 | Hs 29511 | ESTs | |
| 3624 | 23 | AA454546 | Hs 9357 | EST | |
| 33064 | 23 | AA454547 | Hs 9357 | EST | |
| 11175 | 23 | AA454548 | Hs 9357 | EST | |
| 19198 | 23 | AA454549 | Hs 9357 | EST | |
| 5648 | 23 | AA454550 | Hs 9357 | EST | |
| 24247 | 23 | AA454551 | Hs 9357 | EST | |
| 43279 | 23 | AA454552 | Hs 9357 | EST | |
| 22029 | 23 | AA454553 | Hs 9357 | EST | |
| 41987 | 23 | AA454554 | Hs 9357 | EST | |
| 31120 | 23 | AA454555 | Hs 9357 | EST | |
| 6381 | 23 | AA454556 | Hs 9357 | EST | |
| 19283 | 23 | AA454557 | Hs 9357 | EST | |
| 21167 | 23 | AA454558 | Hs 9357 | EST | |
| 32023 | 23 | AA454559 | Hs 9357 | EST | |
| 4871 | 23 | AA454560 | Hs 9357 | EST | |
| 41428 | 23 | AA454561 | Hs 9357 | EST | |
| 31968 | 23 | AA454562 | Hs 9357 | EST | |
| 21962 | 23 | AA454563 | Hs 9357 | EST | |
| 41355 | 23 | AA454564 | Hs 9357 | EST | |
| 40585 | 23 | AA454565 | Hs 9357 | EST | |
| 5307 | 23 | AA454566 | Hs 9357 | EST | |
| 34146 | 23 | AA454567 | Hs 9357 | EST | |
| 8675 | 23 | AA454568 | Hs 9357 | EST | |
| 7347 | 23 | AA454569 | Hs 9357 | EST | |
| 18018 | 23 | AA454570 | Hs 9357 | EST | |
| 25043 | 23 | AA454571 | Hs 9357 | EST | |
| 20294 | 23 | AA454572 | Hs 9357 | EST | |
| 41146 | 23 | AA454573 | Hs 9357 | EST | |
| 34568 | 23 | AA454574 | Hs 9357 | EST | |
| 23105 | 23 | AA454575 | Hs 9357 | EST | |
| 561 | 23 | AA454576 | Hs 9357 | EST | |
| 20042 | 23 | AA454577 | Hs 9357 | EST | |
| 20043 | 23 | AA454578 | Hs 9357 | EST | |

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FIGURE 3 (CONT.)

| | | | |
|----|----------|------|--|
| 21 | AQ72584 | EST | |
| 21 | AA31381 | ESTs | |
| 21 | Hs 55319 | ESTs | |
| 21 | Hs 55320 | ESTs | |
| 21 | Hs 55321 | ESTs | |
| 21 | Hs 55322 | ESTs | |
| 21 | Hs 55323 | ESTs | |
| 21 | Hs 55324 | ESTs | |
| 21 | Hs 55325 | ESTs | |
| 21 | Hs 55326 | ESTs | |
| 21 | Hs 55327 | ESTs | |
| 21 | Hs 55328 | ESTs | |
| 21 | Hs 55329 | ESTs | |
| 21 | Hs 55330 | ESTs | |
| 21 | Hs 55331 | ESTs | |
| 21 | Hs 55332 | ESTs | |
| 21 | Hs 55333 | ESTs | |
| 21 | Hs 55334 | ESTs | |
| 21 | Hs 55335 | ESTs | |
| 21 | Hs 55336 | ESTs | |
| 21 | Hs 55337 | ESTs | |
| 21 | Hs 55338 | ESTs | |
| 21 | Hs 55339 | ESTs | |
| 21 | Hs 55340 | ESTs | |
| 21 | Hs 55341 | ESTs | |
| 21 | Hs 55342 | ESTs | |
| 21 | Hs 55343 | ESTs | |
| 21 | Hs 55344 | ESTs | |
| 21 | Hs 55345 | ESTs | |
| 21 | Hs 55346 | ESTs | |
| 21 | Hs 55347 | ESTs | |
| 21 | Hs 55348 | ESTs | |
| 21 | Hs 55349 | ESTs | |
| 21 | Hs 55350 | ESTs | |
| 21 | Hs 55351 | ESTs | |
| 21 | Hs 55352 | ESTs | |
| 21 | Hs 55353 | ESTs | |
| 21 | Hs 55354 | ESTs | |
| 21 | Hs 55355 | ESTs | |
| 21 | Hs 55356 | ESTs | |
| 21 | Hs 55357 | ESTs | |
| 21 | Hs 55358 | ESTs | |
| 21 | Hs 55359 | ESTs | |
| 21 | Hs 55360 | ESTs | |
| 21 | Hs 55361 | ESTs | |
| 21 | Hs 55362 | ESTs | |
| 21 | Hs 55363 | ESTs | |
| 21 | Hs 55364 | ESTs | |
| 21 | Hs 55365 | ESTs | |
| 21 | Hs 55366 | ESTs | |
| 21 | Hs 55367 | ESTs | |
| 21 | Hs 55368 | ESTs | |
| 21 | Hs 55369 | ESTs | |
| 21 | Hs 55370 | ESTs | |
| 21 | Hs 55371 | ESTs | |
| 21 | Hs 55372 | ESTs | |
| 21 | Hs 55373 | ESTs | |
| 21 | Hs 55374 | ESTs | |
| 21 | Hs 55375 | ESTs | |
| 21 | Hs 55376 | ESTs | |
| 21 | Hs 55377 | ESTs | |
| 21 | Hs 55378 | ESTs | |
| 21 | Hs 55379 | ESTs | |
| 21 | Hs 55380 | ESTs | |
| 21 | Hs 55381 | ESTs | |
| 21 | Hs 55382 | ESTs | |
| 21 | Hs 55383 | ESTs | |
| 21 | Hs 55384 | ESTs | |
| 21 | Hs 55385 | ESTs | |
| 21 | Hs 55386 | ESTs | |
| 21 | Hs 55387 | ESTs | |
| 21 | Hs 55388 | ESTs | |
| 21 | Hs 55389 | ESTs | |
| 21 | Hs 55390 | ESTs | |
| 21 | Hs 55391 | ESTs | |
| 21 | Hs 55392 | ESTs | |
| 21 | Hs 55393 | ESTs | |
| 21 | Hs 55394 | ESTs | |
| 21 | Hs 55395 | ESTs | |
| 21 | Hs 55396 | ESTs | |
| 21 | Hs 55397 | ESTs | |
| 21 | Hs 55398 | ESTs | |
| 21 | Hs 55399 | ESTs | |
| 21 | Hs 55400 | ESTs | |
| 21 | Hs 55401 | ESTs | |
| 21 | Hs 55402 | ESTs | |
| 21 | Hs 55403 | ESTs | |
| 21 | Hs 55404 | ESTs | |
| 21 | Hs 55405 | ESTs | |
| 21 | Hs 55406 | ESTs | |
| 21 | Hs 55407 | ESTs | |
| 21 | Hs 55408 | ESTs | |
| 21 | Hs 55409 | ESTs | |
| 21 | Hs 55410 | ESTs | |
| 21 | Hs 55411 | ESTs | |
| 21 | Hs 55412 | ESTs | |
| 21 | Hs 55413 | ESTs | |
| 21 | Hs 55414 | ESTs | |
| 21 | Hs 55415 | ESTs | |
| 21 | Hs 55416 | ESTs | |
| 21 | Hs 55417 | ESTs | |
| 21 | Hs 55418 | ESTs | |
| 21 | Hs 55419 | ESTs | |
| 21 | Hs 55420 | ESTs | |
| 21 | Hs 55421 | ESTs | |
| 21 | Hs 55422 | ESTs | |
| 21 | Hs 55423 | ESTs | |
| 21 | Hs 55424 | ESTs | |
| 21 | Hs 55425 | ESTs | |
| 21 | Hs 55426 | ESTs | |
| 21 | Hs 55427 | ESTs | |
| 21 | Hs 55428 | ESTs | |
| 21 | Hs 55429 | ESTs | |
| 21 | Hs 55430 | ESTs | |
| 21 | Hs 55431 | ESTs | |
| 21 | Hs 55432 | ESTs | |
| 21 | Hs 55433 | ESTs | |

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FIGURE 4

| Primary Key | Accession | Protein | Origin | Description |
|-------------|-----------|-----------|---|-------------|
| 33015 | U03720 | HA 55278 | Proteasome inhibitor 5 (Prosp) | |
| 19377 | U03573 | HA 15440 | Memo spore core 2397 | |
| 19387 | U03018 | HA 52018 | Memo spore core 2397 | |
| 8125 | AA320711 | HA 52011 | Human primateymer phospholipase (pLPP-1) mRNA partial sequence | |
| 18062 | AA320912 | HA 12013 | Ribonuclease L (2'-5'-phosphodiesterase symplectin-dependent) inhibitor | |
| 18063 | U03018 | HA 52018 | Memo spore core 2397 | |
| 18028 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39659 | AA596468 | HA 74002 | Human mRNA for transposon activator NSM70 complete cds | |
| 39666 | AA596468 | HA 101074 | ESTs | |
| 39667 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39668 | U03018 | HA 52018 | Memo spore core 2397 | |
| 8106 | U03018 | HA 52018 | Memo spore core 2397 | |
| 8648 | AA480119 | HA 65423 | Homo sapiens serum protease inhibitor (Hs) mRNA complete cds | |
| 9619 | U14850 | HA 2711 | HISTONE H2A.X | |
| 9620 | U14850 | HA 2711 | HISTONE H2A.X | |
| 37077 | AA480230 | HA 65384 | Homo sapiens serum protease inhibitor (Hs) mRNA complete cds | |
| 11561 | U03018 | HA 10222 | Est-1 | |
| 16490 | AA320912 | HA 91558 | ESTs | |
| 16491 | AA320912 | HA 91558 | ESTs | |
| 16492 | AA320912 | HA 91558 | ESTs | |
| 12480 | AA451118 | HA 74014 | Phospholipase C beta 4 | |
| 2144 | U14749 | HA 17396 | ESTs | |
| 17443 | AA390081 | HA 17396 | ESTs | |
| 39655 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39656 | U03018 | HA 52018 | Memo spore core 2397 | |
| 6449 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39657 | U03018 | HA 52018 | Memo spore core 2397 | |
| 1802 | U19181 | HA 11980 | ESTs | |
| 19377 | U03018 | HA 52018 | Memo spore core 2397 | |
| 12047 | U03018 | HA 52018 | Memo spore core 2397 | |
| 5002 | U03018 | HA 52018 | Memo spore core 2397 | |
| 33794 | U03018 | HA 52018 | Memo spore core 2397 | |
| 13136 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39179 | U03018 | HA 52018 | Memo spore core 2397 | |
| 17987 | U03018 | HA 52018 | Memo spore core 2397 | |
| 39658 | U03018 | HA 52018 | Memo spore core 2397 | |
| 10333 | U03018 | HA 52018 | Memo spore core 2397 | |
| 1345 | U03018 | HA 52018 | Memo spore core 2397 | |
| 36962 | U03018 | HA 52018 | Memo spore core 2397 | |
| 9510 | U03018 | HA 52018 | Memo spore core 2397 | |
| 17734 | U03018 | HA 52018 | Memo spore core 2397 | |
| 36371 | U03018 | HA 52018 | Memo spore core 2397 | |
| 469 | U03018 | HA 52018 | Memo spore core 2397 | |
| 14254 | U03018 | HA 52018 | Memo spore core 2397 | |
| 5021 | U03018 | HA 52018 | Memo spore core 2397 | |
| 4594 | U03018 | HA 52018 | Memo spore core 2397 | |

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| 134313 | 134359 | 134370 | 134371 | 134372 | 134373 | 134374 | 134375 | 134376 | 134377 | 134378 | 134379 | 134380 | 134381 | 134382 | 134383 | 134384 | 134385 | 134386 | 134387 | 134388 | 134389 | 134390 | 134391 | 134392 | 134393 | 134394 | 134395 | 134396 | 134397 | 134398 | 134399 | 134400 | 134401 | 134402 | 134403 | 134404 | 134405 | 134406 | 134407 | 134408 | 134409 | 134410 | 134411 | 134412 | 134413 | 134414 | 134415 | 134416 | 134417 | 134418 | 134419 | 134420 | 134421 | 134422 | 134423 | 134424 | 134425 | 134426 | 134427 | 134428 | 134429 | 134430 | 134431 | 134432 | 134433 | 134434 | 134435 | 134436 | 134437 | 134438 | 134439 | 134440 | 134441 | 134442 | 134443 | 134444 | 134445 | 134446 | 134447 | 134448 | 134449 | 134450 | 134451 | 134452 | 134453 | 134454 | 134455 | 134456 | 134457 | 134458 | 134459 | 134460 | 134461 | 134462 | 134463 | 134464 | 134465 | 134466 | 134467 | 134468 | 134469 | 134470 | 134471 | 134472 | 134473 | 134474 | 134475 | 134476 | 134477 | 134478 | 134479 | 134480 | 134481 | 134482 | 134483 | 134484 | 134485 | 134486 | 134487 | 134488 | 134489 | 134490 | 134491 | 134492 | 134493 | 134494 | 134495 | 134496 | 134497 | 134498 | 134499 | 134500 | 134501 | 134502 | 134503 | 134504 | 134505 | 134506 | 134507 | 134508 | 134509 | 134510 | 134511 | 134512 | 134513 | 134514 | 134515 | 134516 | 134517 | 134518 | 134519 | 134520 | 134521 | 134522 | 134523 | 134524 | 134525 | 134526 | 134527 | 134528 | 134529 | 134530 | 134531 | 134532 | 134533 | 134534 | 134535 | 134536 | 134537 | 134538 | 134539 | 134540 | 134541 | 134542 | 134543 | 134544 | 134545 | 134546 | 134547 | 134548 | 134549 | 134550 | 134551 | 134552 | 134553 | 134554 | 134555 | 134556 | 134557 | 134558 | 134559 | 134560 | 134561 | 134562 | 134563 | 134564 | 134565 | 134566 | 134567 | 134568 | 134569 | 134570 | 134571 | 134572 | 134573 | 134574 | 134575 | 134576 | 134577 | 134578 | 134579 | 134580 | 134581 | 134582 | 134583 | 134584 | 134585 | 134586 | 134587 | 134588 | 134589 | 134590 | 134591 | 134592 | 134593 | 134594 | 134595 | 134596 | 134597 | 134598 | 134599 | 134600 | 134601 | 134602 | 134603 | 134604 | 134605 | 134606 | 134607 | 134608 | 134609 | 134610 | 134611 | 134612 | 134613 | 134614 | 134615 | 134616 | 134617 | 134618 | 134619 | 134620 | 134621 | 134622 | 134623 | 134624 | 134625 | 134626 | 134627 | 134628 | 134629 | 134630 | 134631 | 134632 | 134633 | 134634 | 134635 | 134636 | 134637 | 134638 | 134639 | 134640 | 134641 | 134642 | 134643 | 134644 | 134645 | 134646 | 134647 | 134648 | 134649 | 134650 | 134651 | 134652 | 134653 | 134654 | 134655 | 134656 | 134657 | 134658 | 134659 | 134660 | 134661 | 134662 | 134663 | 134664 | 134665 | 134666 | 134667 | 134668 | 134669 | 134670 | 134671 | 134672 | 134673 | 134674 | 134675 | 134676 | 134677 | 134678 | 134679 | 134680 | 134681 | 134682 | 134683 | 134684 | 134685 | 134686 | 134687 | 134688 | 134689 | 134690 | 134691 | 134692 | 134693 | 134694 | 134695 | 134696 | 134697 | 134698 | 134699 | 134700 | 134701 | 134702 | 134703 | 134704 | 134705 | 134706 | 134707 | 134708 | 134709 | 134710 | 134711 | 134712 | 134713 | 134714 | 134715 | 134716 | 134717 | 134718 | 134719 | 134720 | 134721 | 134722 | 134723 | 134724 | 134725 | 134726 | 134727 | 134728 | 134729 | 134730 | 134731 | 134732 | 134733 | 134734 | 134735 | 134736 | 134737 | 134738 | 134739 | 134740 | 134741 | 134742 | 134743 | 134744 | 134745 | 134746 | 134747 | 134748 | 134749 | 134750 | 134751 | 134752 | 134753 | 134754 | 134755 | 134756 | 134757 | 134758 | 134759 | 134760 | 134761 | 134762 | 134763 | 134764 | 134765 | 134766 | 134767 | 134768 | 134769 | 134770 | 134771 | 134772 | 134773 | 134774 | 134775 | 134776 | 134777 | 134778 | 134779 | 134780 | 134781 | 134782 | 134783 | 134784 | 134785 | 134786 | 134787 | 134788 | 134789 | 134790 | 134791 | 134792 | 134793 | 134794 | 134795 | 134796 | 134797 | 134798 | 134799 | 134800 | 134801 | 134802 | 134803 | 134804 | 134805 | 134806 | 134807 | 134808 | 134809 | 134810 | 134811 | 134812 | 134813 | 134814 | 134815 | 134816 | 134817 | 134818 | 134819 | 134820 | 134821 | 134822 | 134823 | 134824 | 134825 | 134826 | 134827 | 134828 | 134829 | 134830 | 134831 | 134832 | 134833 | 134834 | 134835 | 134836 | 134837 | 134838 | 134839 | 134840 | 134841 | 134842 | 134843 | 134844 | 134845 | 134846 | 134847 | 134848 | 134849 | 134850 | 134851 | 134852 | 134853 | 134854 | 134855 | 134856 | 134857 | 134858 | 134859 | 134860 | 134861 | 134862 | 134863 | 134864 | 134865 | 134866 | 134867 | 134868 | 134869 | 134870 | 134871 | 134872 | 134873 | 134874 | 134875 | 134876 | 134877 | 134878 | 134879 | 134880 | 134881 | 134882 | 134883 | 134884 | 134885 | 134886 | 134887 | 134888 | 134889 | 134890 | 134891 | 134892 | 134893 | 134894 | 134895 | 134896 | 134897 | 134898 | 134899 | 134900 | 134901 | 134902 | 134903 | 134904 | 134905 | 134906 | 134907 | 134908 | 134909 | 134910 | 134911 | 134912 | 134913 | 134914 | 134915 | 134916 | 134917 | 134918 | 134919 | 134920 | 134921 | 134922 | 134923 | 134924 | 134925 | 134926 | 134927 | 134928 | 134929 | 134930 | 134931 | 134932 | 134933 | 134934 | 134935 | 134936 | 134937 | 134938 | 134939 | 134940 | 134941 | 134942 | 134943 | 134944 | 134945 | 134946 | 134947 | 134948 | 134949 | 134950 | 134951 | 134952 | 134953 | 134954 | 134955 | 134956 | 134957 | 134958 | 134959 | 134960 | 134961 | 134962 | 134963 | 134964 | 134965 | 134966 | 134967 | 134968 | 134969 | 134970 | 134971 | 134972 | 134973 | 134974 | 134975 | 134976 | 134977 | 134978 | 134979 | 134980 | 134981 | 134982 | 134983 | 134984 | 134985 | 134986 | 134987 | 134988 | 134989 | 134990 | 134991 | 134992 | 134993 | 134994 | 134995 | 134996 | 134997 | 134998 | 134999 | 135000 |
| Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | Proteinase inhibitor 5 (pancreas) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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[illegible]

WO 00/55633

PCT/US00/07044

FIGURE 4 (CONT.)

| | | | |
|--------|----|-----------|---|
| 296218 | 10 | AA320411 | Hs 47229 EST: highly similar to R55 RIBOSOMAL PROTEIN L30 (Rane coryza) |
| 402024 | 10 | HE256 | EST: RC_4438306 |
| 8164 | 10 | H1039 | Hs 32080 EST |
| 32464 | 10 | AA320410 | Hs 30404 Human mRNA for R54A101 gene complete cds |
| 6963 | 10 | AA320410 | AF1424-INTERM1107_M |
| 35332 | 10 | AA320410 | Hs 37105 Human mRNA for C12C3 |
| 27310 | 10 | H23P-H137 | Hs 36523 EST |
| 36652 | 10 | AA41027 | Hs 36523 EST |
| 28974 | 10 | AA320504 | Hs 36523 EST |
| 37179 | 10 | AA320504 | Hs 36523 EST |
| 4662 | 10 | U6347 | Hs 36523 EST |
| 28700 | 10 | AA320197 | Hs 36523 EST |
| 40061 | 10 | AA320197 | Hs 36523 EST |
| 17541 | 10 | AA17449 | Hs 36523 EST |
| 19449 | 10 | H7803 | Hs 36523 EST |
| 28918 | 10 | AA320303 | Hs 36523 EST |
| 34186 | 10 | AA320303 | Hs 36523 EST |
| 29229 | 10 | H4845 | Hs 36523 EST |
| 32189 | 10 | AA320310 | Hs 36523 EST |
| 30739 | 10 | AA320310 | Hs 36523 EST |
| 21910 | 10 | H66831 | Hs 36523 EST |
| 21962 | 10 | AA320310 | Hs 36523 EST |
| 25925 | 10 | AA104484 | Hs 36523 EST |
| 22044 | 10 | H66831 | Hs 36523 EST |
| 218 | 10 | H66831 | Hs 36523 EST |
| 28100 | 10 | AA320305 | Hs 36523 EST |
| 40329 | 10 | H66831 | Hs 36523 EST |
| 8713 | 10 | V0564 | Hs 36523 EST |
| 33377 | 10 | V0564 | Hs 36523 EST |
| 29718 | 10 | AA320310 | Hs 36523 EST |
| 21558 | 10 | AA320310 | Hs 36523 EST |
| 40113 | 10 | H7803 | Hs 36523 EST |
| 37491 | 10 | AA430239 | Hs 36523 EST |
| 354 | 10 | D14657 | Hs 36523 EST |
| 29983 | 10 | H97819 | Hs 36523 EST |
| 34863 | 10 | AA430239 | Hs 36523 EST |
| 39402 | 10 | D51091 | Hs 36523 EST |
| 17903 | 10 | AA430239 | Hs 36523 EST |
| 22047 | 10 | H65943 | Hs 36523 EST |
| 4676 | 10 | U52008 | Hs 36523 EST |
| 39294 | 10 | AA430239 | Hs 36523 EST |
| 3208 | 10 | U11218 | Hs 36523 EST |

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| | | | |
|-----|----------|-----------|--|
| 16 | M25725 | Hs 25902 | Crutin B1 |
| 17 | M25726 | Hs 54952 | Crutin B1 |
| 18 | M25727 | Hs 113919 | ES1 |
| 19 | M25728 | Hs 156333 | Homo sapiens clone 2022 mRNA sequence |
| 20 | M25729 | Hs 84713 | Human hungenin interacting protein (H2F) mRNA complete cds |
| 21 | M25730 | Hs 82609 | Hydroxyhengenin interacting protein (H2F) mRNA complete cds |
| 22 | M25731 | Hs 82610 | Hydroxyhengenin interacting protein (H2F) mRNA complete cds |
| 23 | M25732 | Hs 12189 | Human mRNA for UDO'-specific vasodilator complete cds |
| 24 | M11162 | Hs 78781 | Peritoneal mesothelial protein 1 (P203 Zebrafish syndrome) |
| 25 | R01136 | Hs 20331 | ES1.1 moderately similar to H-gene phosphoprotein 11 [J. Spatny] |
| 26 | M25733 | Hs 93063 | ES17 |
| 27 | M25734 | Hs 105965 | ES17 |
| 28 | AA069564 | Hs 93064 | ES17 |
| 29 | N23306 | Hs 93065 | ES17 |
| 30 | M25735 | Hs 31695 | ES1 - H46317 |
| 31 | M25736 | Hs 31696 | ES1 - H46317 |
| 32 | H32021 | Hs 85045 | ES17 |
| 33 | AA14327 | Hs 85046 | ES17 |
| 34 | N24184 | Hs 43511 | ES1 - H43511 |
| 35 | H32022 | Hs 43512 | ES1 - H43511 |
| 36 | H32023 | Hs 43513 | ES1 - H43511 |
| 37 | H32024 | Hs 43514 | ES1 - H43511 |
| 38 | H32025 | Hs 43515 | ES1 - H43511 |
| 39 | H32026 | Hs 43516 | ES1 - H43511 |
| 40 | H32027 | Hs 43517 | ES1 - H43511 |
| 41 | H32028 | Hs 43518 | ES1 - H43511 |
| 42 | H32029 | Hs 43519 | ES1 - H43511 |
| 43 | H32030 | Hs 43520 | ES1 - H43511 |
| 44 | H32031 | Hs 43521 | ES1 - H43511 |
| 45 | H32032 | Hs 43522 | ES1 - H43511 |
| 46 | H32033 | Hs 43523 | ES1 - H43511 |
| 47 | H32034 | Hs 43524 | ES1 - H43511 |
| 48 | H32035 | Hs 43525 | ES1 - H43511 |
| 49 | H32036 | Hs 43526 | ES1 - H43511 |
| 50 | H32037 | Hs 43527 | ES1 - H43511 |
| 51 | H32038 | Hs 43528 | ES1 - H43511 |
| 52 | H32039 | Hs 43529 | ES1 - H43511 |
| 53 | H32040 | Hs 43530 | ES1 - H43511 |
| 54 | H32041 | Hs 43531 | ES1 - H43511 |
| 55 | H32042 | Hs 43532 | ES1 - H43511 |
| 56 | H32043 | Hs 43533 | ES1 - H43511 |
| 57 | H32044 | Hs 43534 | ES1 - H43511 |
| 58 | H32045 | Hs 43535 | ES1 - H43511 |
| 59 | H32046 | Hs 43536 | ES1 - H43511 |
| 60 | H32047 | Hs 43537 | ES1 - H43511 |
| 61 | H32048 | Hs 43538 | ES1 - H43511 |
| 62 | H32049 | Hs 43539 | ES1 - H43511 |
| 63 | H32050 | Hs 43540 | ES1 - H43511 |
| 64 | H32051 | Hs 43541 | ES1 - H43511 |
| 65 | H32052 | Hs 43542 | ES1 - H43511 |
| 66 | H32053 | Hs 43543 | ES1 - H43511 |
| 67 | H32054 | Hs 43544 | ES1 - H43511 |
| 68 | H32055 | Hs 43545 | ES1 - H43511 |
| 69 | H32056 | Hs 43546 | ES1 - H43511 |
| 70 | H32057 | Hs 43547 | ES1 - H43511 |
| 71 | H32058 | Hs 43548 | ES1 - H43511 |
| 72 | H32059 | Hs 43549 | ES1 - H43511 |
| 73 | H32060 | Hs 43550 | ES1 - H43511 |
| 74 | H32061 | Hs 43551 | ES1 - H43511 |
| 75 | H32062 | Hs 43552 | ES1 - H43511 |
| 76 | H32063 | Hs 43553 | ES1 - H43511 |
| 77 | H32064 | Hs 43554 | ES1 - H43511 |
| 78 | H32065 | Hs 43555 | ES1 - H43511 |
| 79 | H32066 | Hs 43556 | ES1 - H43511 |
| 80 | H32067 | Hs 43557 | ES1 - H43511 |
| 81 | H32068 | Hs 43558 | ES1 - H43511 |
| 82 | H32069 | Hs 43559 | ES1 - H43511 |
| 83 | H32070 | Hs 43560 | ES1 - H43511 |
| 84 | H32071 | Hs 43561 | ES1 - H43511 |
| 85 | H32072 | Hs 43562 | ES1 - H43511 |
| 86 | H32073 | Hs 43563 | ES1 - H43511 |
| 87 | H32074 | Hs 43564 | ES1 - H43511 |
| 88 | H32075 | Hs 43565 | ES1 - H43511 |
| 89 | H32076 | Hs 43566 | ES1 - H43511 |
| 90 | H32077 | Hs 43567 | ES1 - H43511 |
| 91 | H32078 | Hs 43568 | ES1 - H43511 |
| 92 | H32079 | Hs 43569 | ES1 - H43511 |
| 93 | H32080 | Hs 43570 | ES1 - H43511 |
| 94 | H32081 | Hs 43571 | ES1 - H43511 |
| 95 | H32082 | Hs 43572 | ES1 - H43511 |
| 96 | H32083 | Hs 43573 | ES1 - H43511 |
| 97 | H32084 | Hs 43574 | ES1 - H43511 |
| 98 | H32085 | Hs 43575 | ES1 - H43511 |
| 99 | H32086 | Hs 43576 | ES1 - H43511 |
| 100 | H32087 | Hs 43577 | ES1 - H43511 |
| 101 | H32088 | Hs 43578 | ES1 - H43511 |
| 102 | H32089 | Hs 43579 | ES1 - H43511 |
| 103 | H32090 | Hs 43580 | ES1 - H43511 |
| 104 | H32091 | Hs 43581 | ES1 - H43511 |
| 105 | H32092 | Hs 43582 | ES1 - H43511 |
| 106 | H32093 | Hs 43583 | ES1 - H43511 |
| 107 | H32094 | Hs 43584 | ES1 - H43511 |
| 108 | H32095 | Hs 43585 | ES1 - H43511 |
| 109 | H32096 | Hs 43586 | ES1 - H43511 |
| 110 | H32097 | Hs 43587 | ES1 - H43511 |
| 111 | H32098 | Hs 43588 | ES1 - H43511 |
| 112 | H32099 | Hs 43589 | ES1 - H43511 |
| 113 | H32100 | Hs 43590 | ES1 - H43511 |
| 114 | H32101 | Hs 43591 | ES1 - H43511 |
| 115 | H32102 | Hs 43592 | ES1 - H43511 |
| 116 | H32103 | Hs 43593 | ES1 - H43511 |
| 117 | H32104 | Hs 43594 | ES1 - H43511 |
| 118 | H32105 | Hs 43595 | ES1 - H43511 |
| 119 | H32106 | Hs 43596 | ES1 - H43511 |
| 120 | H32107 | Hs 43597 | ES1 - H43511 |
| 121 | H32108 | Hs 43598 | ES1 - H43511 |
| 122 | H32109 | Hs 43599 | ES1 - H43511 |
| 123 | H32110 | Hs 43600 | ES1 - H43511 |
| 124 | H32111 | Hs 43601 | ES1 - H43511 |
| 125 | H32112 | Hs 43602 | ES1 - H43511 |
| 126 | H32113 | Hs 43603 | ES1 - H43511 |
| 127 | H32114 | Hs 43604 | ES1 - H43511 |
| 128 | H32115 | Hs 43605 | ES1 - H43511 |
| 129 | H32116 | Hs 43606 | ES1 - H43511 |
| 130 | H32117 | Hs 43607 | ES1 - H43511 |
| 131 | H32118 | Hs 43608 | ES1 - H43511 |
| 132 | H32119 | Hs 43609 | ES1 - H43511 |
| 133 | H32120 | Hs 43610 | ES1 - H43511 |
| 134 | H32121 | Hs 43611 | ES1 - H43511 |
| 135 | H32122 | Hs 43612 | ES1 - H43511 |
| 136 | H32123 | Hs 43613 | ES1 - H43511 |
| 137 | H32124 | Hs 43614 | ES1 - H43511 |
| 138 | H32125 | Hs 43615 | ES1 - H43511 |
| 139 | H32126 | Hs 43616 | ES1 - H43511 |
| 140 | H32127 | Hs 43617 | ES1 - H43511 |
| 141 | H32128 | Hs 43618 | ES1 - H43511 |
| 142 | H32129 | Hs 43619 | ES1 - H43511 |
| 143 | H32130 | Hs 43620 | ES1 - H43511 |
| 144 | H32131 | Hs 43621 | ES1 - H43511 |
| 145 | H32132 | Hs 43622 | ES1 - H43511 |
| 146 | H32133 | Hs 43623 | ES1 - H43511 |
| 147 | H32134 | Hs 43624 | ES1 - H43511 |
| 148 | H32135 | Hs 43625 | ES1 - H43511 |
| 149 | H32136 | Hs 43626 | ES1 - H43511 |
| 150 | H32137 | Hs 43627 | ES1 - H43511 |
| 151 | H32138 | Hs 43628 | ES1 - H43511 |
| 152 | H32139 | Hs 43629 | ES1 - H43511 |
| 153 | H32140 | Hs 43630 | ES1 - H43511 |
| 154 | H32141 | Hs 43631 | ES1 - H43511 |
| 155 | H32142 | Hs 43632 | ES1 - H43511 |
| 156 | H32143 | Hs 43633 | ES1 - H43511 |
| 157 | H32144 | Hs 43634 | ES1 - H43511 |
| 158 | H32145 | Hs 43635 | ES1 - H43511 |
| 159 | H32146 | Hs 43636 | ES1 - H43511 |
| 160 | H32147 | Hs 43637 | ES1 - H43511 |
| 161 | H32148 | Hs 43638 | ES1 - H43511 |
| 162 | H32149 | Hs 43639 | ES1 - H43511 |
| 163 | H32150 | Hs 43640 | ES1 - H43511 |
| 164 | H32151 | Hs 43641 | ES1 - H43511 |
| 165 | H32152 | Hs 43642 | ES1 - H43511 |
| 166 | H32153 | Hs 43643 | ES1 - H43511 |
| 167 | H32154 | Hs 43644 | ES1 - H43511 |
| 168 | H32155 | Hs 43645 | ES1 - H43511 |
| 169 | H32156 | Hs 43646 | ES1 - H43511 |
| 170 | H32157 | Hs 43647 | ES1 - H43511 |
| 171 | H32158 | Hs 43648 | ES1 - H43511 |
| 172 | H32159 | Hs 43649 | ES1 - H43511 |
| 173 | H32160 | Hs 43650 | ES1 - H43511 |
| 174 | H32161 | Hs 43651 | ES1 - H43511 |
| 175 | H32162 | Hs 43652 | ES1 - H43511 |
| 176 | H32163 | Hs 43653 | ES1 - H43511 |
| 177 | H32164 | Hs 43654 | ES1 - H43511 |
| 178 | H32165 | Hs 43655 | ES1 - H43511 |
| 179 | H32166 | Hs 43656 | ES1 - H43511 |
| 180 | H32167 | Hs 43657 | ES1 - H43511 |
| 181 | H32168 | Hs 43658 | ES1 - H43511 |
| 182 | H32169 | Hs 43659 | ES1 - H43511 |
| 183 | H32170 | Hs 43660 | ES1 - H43511 |
| 184 | H32171 | Hs 43661 | ES1 - H43511 |
| 185 | H32172 | Hs 43662 | ES1 - H43511 |
| 186 | H32173 | Hs 43663 | ES1 - H43511 |
| 187 | H32174 | Hs 43664 | ES1 - H43511 |
| 188 | H32175 | Hs 43665 | ES1 - H43511 |
| 189 | H32176 | Hs 43666 | ES1 - H43511 |
| 190 | H32177 | Hs 43667 | ES1 - H43511 |
| 191 | H32178 | Hs 43668 | ES1 - H43511 |
| 192 | H32179 | Hs 43669 | ES1 - H43511 |
| 193 | H32180 | Hs 43670 | ES1 - H43511 |
| 194 | H32181 | Hs 43671 | ES1 - H43511 |
| 195 | H32182 | Hs 43672 | ES1 - H43511 |
| 196 | H32183 | Hs 43673 | ES1 - H43511 |
| 197 | H32184 | Hs 43674 | ES1 - H43511 |
| 198 | H32185 | Hs 43675 | ES1 - H43511 |
| 199 | H32186 | Hs 43676 | ES1 - H43511 |
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| 201 | H32188 | Hs 43678 | ES1 - H43511 |
| 202 | H32189 | Hs 43679 | ES1 - H43511 |
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| 204 | H32191 | Hs 43681 | ES1 - H43511 |
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| 206 | H32193 | Hs 43683 | ES1 - H43511 |
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| 210 | H32197 | Hs 43687 | ES1 - H43511 |
| 211 | H32198 | Hs 43688 | ES1 - H43511 |
| 212 | H32199 | Hs 43689 | ES1 - H43511 |
| 213 | H32200 | Hs 43690 | ES1 - H43511 |
| 214 | H32201 | Hs 43691 | ES1 - H43511 |
| 215 | H32202 | Hs 43692 | ES1 - H43511 |
| 216 | H32203 | Hs 43693 | ES1 - H43511 |
| 217 | H32204 | Hs 43694 | ES1 - H43511 |
| 218 | H32205 | Hs 43695 | ES1 - H43511 |
| 219 | H32206 | Hs 43696 | ES1 - H43511 |
| 220 | H32207 | Hs 43697 | ES1 - H43511 |
| 221 | H32208 | Hs 43698 | ES1 - H43511 |
| 222 | H32209 | Hs 43699 | ES1 - H43511 |
| 223 | H32210 | Hs 43700 | ES1 - H43511 |
| 224 | H32211 | Hs 43701 | ES1 - H43511 |
| 225 | H32212 | Hs 43702 | ES1 - H43511 |
| 226 | H32213 | Hs 43703 | ES1 - H43511 |
| 227 | H32214 | Hs 43704 | ES1 - H43511 |
| 228 | H32215 | Hs 43705 | ES1 - H43511 |
| 229 | H32216 | Hs 43706 | ES1 - H43511 |
| 230 | H32217 | Hs 43707 | ES1 - H43511 |
| 231 | H32218 | Hs 43708 | ES1 - H43511 |
| 232 | H32219 | Hs 43709 | ES1 - H43511 |
| 233 | H32220 | Hs 43710 | ES1 - H43511 |
| 234 | H32221 | Hs 43711 | ES1 - H43511 |
| 235 | H32222 | Hs 43712 | ES1 - H43511 |
| 236 | H32223 | Hs 43713 | ES1 - H43511 |
| 237 | H32224 | Hs 43714 | ES1 - H43511 |
| 238 | H32225 | Hs 43715 | ES1 - H43511 |
| 239 | H32226 | Hs 43716 | ES1 - H43511 |
| 240 | H32227 | Hs 43717 | ES1 - H43511 |
| 241 | H32228 | Hs 43718 | ES1 - H43511 |
| 242 | H32229 | Hs 43719 | ES1 - H43511 |
| 243 | H32230 | Hs 43720 | ES1 - H43511 |
| 244 | H32231 | Hs 43721 | ES1 - H43511 |
| 245 | H32232 | Hs 43722 | ES1 - H43511 |
| 246 | H32233 | Hs 43723 | ES1 - H43511 |
| 247 | H32234 | Hs 43724 | ES1 - H43511 |
| 248 | H32235 | Hs 43725 | ES1 - H43511 |
| 249 | H32236 | Hs 43726 | ES1 - H43511 |
| 250 | H32237 | Hs 43727 | ES1 - H43511 |
| 251 | H32238 | Hs 43728 | ES1 - H43511 |
| 252 | H32239 | Hs 43729 | ES1 - H43511 |
| 253 | H32240 | Hs 43730 | ES1 - H43511 |
| 254 | H32241 | Hs 43731 | ES1 - H43511 |
| 255 | H32242 | Hs 43732 | ES1 - H43511 |
| 256 | H32243 | Hs 43733 | ES1 - H43511 |
| 257 | H32244 | Hs 43734 | ES1 - H43511 |
| 258 | H32245 | Hs 43735 | ES1 - H43511 |
| 259 | H32246 | Hs 43736 | ES1 - H43511 |
| 260 | H32247 | Hs 43737 | ES1 - H43511 |
| 261 | H32248 | Hs 43738 | ES1 - H43511 |
| 262 | H32249 | Hs 43739 | ES1 - H43511 |
| 263 | H32250 | Hs 43740 | ES1 - H43511 |
| 264 | H32251 | Hs 43741 | ES1 - H43511 |
| 265 | H32252 | Hs 43742 | ES1 - H43511 |
| 266 | H32253 | Hs 43743 | ES1 - H43511 |
| 267 | H32254 | Hs 43744 | ES1 - H43511 |
| 268 | H32255 | Hs 43745 | ES1 - H43511 |
| 269 | H32256 | Hs 43746 | ES1 - H43511 |
| 270 | H32257 | Hs 43747 | ES1 - H43511 |
| 271 | H32258 | Hs 43748 | ES1 - H43511 |
| 272 | H32259 | Hs 43749 | ES1 - H43511 |
| 273 | H32260 | Hs 43750 | ES1 - H43511 |
| 274 | H32261 | Hs 43751 | ES1 - H43511 |
| 275 | H32262 | Hs 43752 | |

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FIGURE 4 (CONT.)

| | | | |
|-------|----------|---|--|
| 3042 | AA621523 | Hs 110832 ESTs | |
| 27554 | AA42321 | Hs 81608 ESTs | |
| 15956 | AA49719 | Hs 76395 Human placenta (DMS) mRNA complete cds | |
| 6154 | AA46367 | Hs 110835 EST - RC_AA60607 | |
| 42463 | W61180 | Hs 103130 ESTs | |
| 3769 | W61181 | Hs 103130 ESTs | |
| 31765 | W60703 | Hs 35043 ESTs | |
| 22068 | R98192 | Hs 35048 ESTs | |
| 25240 | AA039713 | Hs 110406 ESTs | |
| 17463 | AA123147 | Hs 64891 ESTs | |
| 16654 | AA05352 | Hs 71922 ESTs | |
| 3769 | U07550 | Hs 1197 | |
| 4991 | U69548 | Hs 83231 | |
| 20416 | N49529 | Hs 32170 ESTs | |
| 27965 | AA470155 | Hs 75897 | |
| 27000 | AA43793 | Hs 84791 ESTs | |
| 24677 | Z36338 | Hs 21201 | |
| 9382 | C99918 | Hs 3386 | |
| 35215 | AA123147 | Hs 64891 | |
| 30209 | AA421306 | Hs 13989 | |
| 20064 | H98953 | Hs 16508 ESTs | |
| 9713 | C44338 | Hs 78484 | |
| 28626 | C11938 | Hs 82945 | |
| 25904 | AA148835 | Hs 111710 ESTs | |
| 14664 | T22296 | Hs 12101 | |
| 25285 | AA043765 | Hs 54549 | |
| 13805 | AA459437 | Hs 22086 | |
| 1544 | J05968 | Hs 2012 | |
| 42311 | T97257 | Hs 54560 ESTs | |
| 2023 | L34600 | Hs 3323 | |
| 30707 | Z26937 | Hs 3301 | |
| 17220 | AA032073 | Hs 85249 | |
| 24322 | W95782 | Hs 18539 ESTs | |
| 8208 | AA471152 | Hs 5101 | |
| 387 | C28549 | Hs 5101 | |
| 12519 | AA396109 | Hs 22090 | |
| 11519 | AA180468 | Hs 33748 ESTs | |
| 16338 | AA228238 | Hs 1191 | |
| 29803 | H28611 | Hs 92911 ESTs | |
| 25955 | AA112308 | Hs 107932 | |
| 34018 | AA191488 | Hs 72614 | |
| 2791 | C14632 | Hs 84728 | |
| 24035 | Z28409 | Hs 85025 | |
| 19127 | AA006069 | Hs 38441 ESTs | |

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459842 Hs 8739 ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PM16, PCT1 INTERGENIC REGION [SACCHAROMYCES CEREVISIAE]

| | | | | |
|-----|----------|-----------|---|---|
| 4 | U023524 | Hs 12476 | EST1 | Weakly similar to ZINC FINGER PROTEIN 51 (H sapiens) |
| 5 | U023524 | Hs 12476 | EST1 | Human Oxytetracycline aminocyclase superfamily (MAG2) mRNA complete cds |
| 6 | X15159 | Hs 17711 | MOO-DEFICIENT METABOLITE TRANSFORMYLASE OF HYDROXYMETHYLGLUTARATE | |
| 7 | AA101046 | Hs 83035 | EST1 | Hs 83035 |
| 8 | U023524 | Hs 83035 | EST1 | Hs 83035 |
| 9 | R14725 | Hs 188403 | ONA-REPAIR PROTEIN (ORC1) | |
| 10 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 11 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 12 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 13 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 14 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 15 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 16 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 17 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 18 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 19 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 20 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 21 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 22 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 23 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 24 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 25 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 26 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 27 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 28 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 29 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 30 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 31 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 32 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 33 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 34 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 35 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 36 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 37 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 38 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 39 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 40 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 41 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 42 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 43 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 44 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 45 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 46 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 47 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 48 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 49 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 50 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 51 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 52 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 53 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 54 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 55 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 56 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 57 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 58 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 59 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 60 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 61 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 62 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 63 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 64 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 65 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 66 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 67 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 68 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 69 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 70 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 71 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 72 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 73 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 74 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 75 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 76 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 77 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 78 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 79 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 80 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 81 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 82 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 83 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 84 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 85 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 86 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 87 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 88 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 89 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 90 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 91 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 92 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 93 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 94 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 95 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 96 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 97 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 98 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 99 | AA101951 | Hs 188600 | EST1 | Hs 188600 |
| 100 | AA101951 | Hs 188600 | EST1 | Hs 188600 |

FIGURE 4 (CONT.)

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FIGURE 4 (CONT.)

[illegible]

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FIGURE 4 (CONT.)

| | | | | | | | |
|-------|----|----------|-----------|--|-----------|----------------------|--|
| 16426 | 21 | H23469 | Hs 13142 | EST | Hs 105761 | Receptor protein LSP | |
| 27784 | 23 | AAH18389 | Hs 42219 | EST1 | Hs 105762 | Receptor protein LSP | |
| 27784 | 23 | AAH18389 | Hs 42219 | EST1 | Hs 105763 | Receptor protein LSP | |
| 13522 | 21 | AAH18389 | Hs 29611 | EST1 | Hs 105764 | Receptor protein LSP | |
| 20253 | 23 | AAH18389 | Hs 142497 | EST1 | Hs 105765 | Receptor protein LSP | |
| 35714 | 23 | U10227 | Hs 50072 | Human hsa-A10 msa-1 (PAC1) cDNA complete cds | Hs 105766 | Receptor protein LSP | |
| 16977 | 23 | AAH4516 | Hs 66843 | EST1 | Hs 105767 | Receptor protein LSP | |
| 5946 | 23 | AAH3327 | Hs 105768 | EST1 | Hs 105768 | Receptor protein LSP | |
| 26247 | 23 | U10227 | Hs 105769 | EST1 | Hs 105769 | Receptor protein LSP | |
| 9239 | 23 | U10227 | Hs 105770 | EST1 | Hs 105770 | Receptor protein LSP | |
| 33695 | 23 | U10227 | Hs 105771 | EST1 | Hs 105771 | Receptor protein LSP | |
| 7404 | 23 | AAH3469 | Hs 105772 | EST1 | Hs 105772 | Receptor protein LSP | |
| 6381 | 23 | AAH3469 | Hs 105773 | EST1 | Hs 105773 | Receptor protein LSP | |
| 2197 | 23 | AAH3469 | Hs 105774 | EST1 | Hs 105774 | Receptor protein LSP | |
| 28203 | 23 | AAH3469 | Hs 105775 | EST1 | Hs 105775 | Receptor protein LSP | |
| 30320 | 23 | AAH3469 | Hs 105776 | EST1 | Hs 105776 | Receptor protein LSP | |
| 11667 | 23 | AAH3469 | Hs 105777 | EST1 | Hs 105777 | Receptor protein LSP | |
| 26550 | 23 | AAH3469 | Hs 105778 | EST1 | Hs 105778 | Receptor protein LSP | |
| 3343 | 23 | AAH3469 | Hs 105779 | EST1 | Hs 105779 | Receptor protein LSP | |
| 5605 | 23 | AAH3469 | Hs 105780 | EST1 | Hs 105780 | Receptor protein LSP | |
| 25756 | 23 | AAH3469 | Hs 105781 | EST1 | Hs 105781 | Receptor protein LSP | |
| 34104 | 22 | AAH3469 | Hs 105782 | EST1 | Hs 105782 | Receptor protein LSP | |
| 7972 | 22 | AAH3469 | Hs 105783 | EST1 | Hs 105783 | Receptor protein LSP | |
| 18516 | 22 | AAH3469 | Hs 105784 | EST1 | Hs 105784 | Receptor protein LSP | |
| 20843 | 22 | AAH3469 | Hs 105785 | EST1 | Hs 105785 | Receptor protein LSP | |
| 30564 | 22 | AAH3469 | Hs 105786 | EST1 | Hs 105786 | Receptor protein LSP | |
| 41546 | 22 | AAH3469 | Hs 105787 | EST1 | Hs 105787 | Receptor protein LSP | |
| 22834 | 22 | AAH3469 | Hs 105788 | EST1 | Hs 105788 | Receptor protein LSP | |
| 36406 | 22 | AAH3469 | Hs 105789 | EST1 | Hs 105789 | Receptor protein LSP | |
| 651 | 22 | AAH3469 | Hs 105790 | EST1 | Hs 105790 | Receptor protein LSP | |
| 20221 | 22 | AAH3469 | Hs 105791 | EST1 | Hs 105791 | Receptor protein LSP | |
| 26656 | 22 | AAH3469 | Hs 105792 | EST1 | Hs 105792 | Receptor protein LSP | |
| 11686 | 22 | AAH3469 | Hs 105793 | EST1 | Hs 105793 | Receptor protein LSP | |
| 30564 | 22 | AAH3469 | Hs 105794 | EST1 | Hs 105794 | Receptor protein LSP | |
| 38341 | 22 | AAH3469 | Hs 105795 | EST1 | Hs 105795 | Receptor protein LSP | |
| 11603 | 22 | AAH3469 | Hs 105796 | EST1 | Hs 105796 | Receptor protein LSP | |
| 30565 | 22 | AAH3469 | Hs 105797 | EST1 | Hs 105797 | Receptor protein LSP | |
| 11900 | 22 | AAH3469 | Hs 105798 | EST1 | Hs 105798 | Receptor protein LSP | |
| 5051 | 22 | AAH3469 | Hs 105799 | EST1 | Hs 105799 | Receptor protein LSP | |
| 20574 | 22 | AAH3469 | Hs 105800 | EST1 | Hs 105800 | Receptor protein LSP | |

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FIGURE 5

| Primary Key | fold down-regulated of Tumor vs | Accession | Unigene CLUSTER | Unigene Descriptor |
|-------------|---------------------------------|-----------|-----------------|--|
| 2340 | >10 | M15656 | Hs.75592 | Aldolase B fructose-bisphosphate |
| 6463 | >10 | XG0908 | Hs.74126 | H-sapiens mRNA for I-18P (I-18AP) protein |
| 42139 | >10 | T73335 | Hs.93194 | APOLIPROTEIN A1 PRECURSOR |
| 4544 | >10 | U48959 | Hs.75690 | H-sapiens mRNA for myosin light chain kinase |
| 1583 | >10 | K02705 | Hs.59512 | COMPLEMENT C3 PRECURSOR |
| 2426 | >10 | M19928 | Hs.595 | Apolipoprotein B (including ApoB) antigen |
| 8959 | >10 | AB002351 | Hs.10387 | Human mRNA for KIAA0353 gene partial cds |
| 24572 | >10 | Z38688 | Hs.24192 | ESTs |
| 17810 | >10 | AA151402 | Hs.46631 | ESTs |
| 7006 | >10 | Z70295 | Hs.32966 | H-sapiens mRNA for GCAP-II/uroguanylin precursor |
| 1304 | >10 | HG4310- | Hs.05424 | EST - HG4310-HT4590 |
| 5980 | >10 | XG4559 | Hs.121713 | Tetranectin (plasminogen-binding protein) |
| 41987 | >10 | T47089 | Hs.121713 | Cytochrome P450 subfamily XXI (stereoid 21-hydroxylase congenital adrenal hyperplasia) |
| 24461 | >10 | W64427 | Hs.3307 | ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus |
| 2372 | >10 | M16594 | Hs.80552 | Glutathione S-transferase A2 |
| 6001 | >10 | X65727 | Hs.80552 | Glutathione S-transferase A2 |
| 1750 | >10 | L10955 | Hs.89485 | Carbolic anhydrase IV |
| 15130 | >10 | U77543 | Hs.95555 | Homo sapiens K12 protein precursor mRNA complete cds |
| 12467 | >10 | AA402656 | Hs.28264 | ESTs |
| 41148 | >10 | R06984 | Hs.50404 | EST - RC_R06984 s |
| 31652 | >10 | N73968 | Hs.50404 | Human chemokine (TECK) mRNA complete cds |
| 4695 | >10 | U61010 | EST - U61010 | ESTs |
| 20359 | >10 | AA609133 | Hs.58115 | ESTs |
| 24066 | >10 | W02505 | Hs.111676 | ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens] |
| 33262 | >10 | W73194 | Hs.80552 | ESTs |
| 12054 | >10 | AA394757 | Hs.21910 | ESTs |
| 41473 | >10 | R48732 | Hs.11006 | ESTs |
| 27106 | >10 | AA404397 | Hs.59414 | ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens] |
| 2848 | >10 | M82896 | Hs.169 | TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR |
| 19537 | >10 | F03270 | Hs.35853 | ESTs |
| 18784 | >10 | P09746 | Hs.7974 | ESTs |
| 5773 | >10 | X54162 | Hs.79386 | 64 KD AUTOANTIGEN D1 |

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FIGURE 5 (CONT.)

| | | | | | |
|-------|-----|----------|-----------|--|--|
| 27387 | >10 | AA426330 | Hs.76204 | ESTs | |
| 2866 | >10 | M59115 | Hs.76682 | Complement component 4A | |
| 42530 | >10 | W72859 | Hs.74669 | ESTs Weakly similar to SYNAPTOTREJUN 2 [H.sapiens] | |
| 877 | >10 | D87133 | Hs.84753 | Human mRNA for KIAA0246 gene partial cds | |
| 850 | >10 | D76014 | Hs.74566 | Human mRNA for dihydropyrimidinase related protein-3 complete cds | |
| 7026 | >10 | Z80345 | Hs.127610 | Acyl-Coenzyme A dehydrogenase C2 to C-3 short chain | |
| 18736 | >10 | AA045306 | Hs.42596 | ESTs | |
| 4630 | >10 | U32101 | Hs.5959 | Human YMP mRNA complete cds | |
| 4655 | >10 | U52569 | Hs.50296 | BRAIN SPECIFIC POLYPEPTIDE PEP-19 | |
| 42758 | >10 | Z41411 | Hs.107040 | ESTs | |
| 35637 | >10 | AA402933 | Hs.28263 | ESTs | |
| 40392 | >10 | H59597 | Hs.108880 | ESTs | |
| 7354 | >10 | AA092348 | Hs.7658 | ESTs | |
| 9034 | >10 | C01833 | Hs.29759 | ESTs Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens] | |
| 10936 | >10 | AA121534 | Hs.6923 | ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus] | |
| 5520 | >10 | X06256 | Hs.119218 | Integrin alpha 5 (fibronectin receptor alpha polypeptide) | |
| 2547 | >10 | I/25009 | Hs.1009 | ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1 | |
| 9003 | >10 | C00008 | Hs.107662 | ESTs | |
| 41628 | >10 | R70212 | Hs.79630 | Immunoglobulin-associated alpha | |
| 21934 | >10 | R44449 | Hs.48778 | ESTs | |
| 11129 | 6 | AA156873 | Hs.15970 | ESTs | |
| 40387 | 7 | H99460 | Hs.108673 | ESTs | |

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FIGURE 6

| Primary Key | Fold downregulated end of Tumor | Accession | Unigene CLUSTER | Unigene Descriptor |
|-------------|---------------------------------|-----------|-------------------|--|
| 2348 | >10 | M15656 | Hs.75592 | Adh5ase B nuclease biophosphate |
| 6403 | >10 | X69008 | Hs.74126 | H.sapiens mRNA for H-SP (HABP) protein |
| 42139 | >10 | T73335 | Hs.93194 | APOLIPROTEIN A1 PRECURSOR |
| 4544 | >10 | U49959 | Hs.75950 | H.sapiens mRNA for myosin light chain kinase |
| 1583 | >10 | K02765 | Hs.59512 | COMPLEMENT C3 PRECURSOR |
| 2426 | >10 | M19828 | Hs.585 | Apolipoprotein B (including ApoB) antigen |
| 8859 | >10 | A8002351 | Hs.10587 | Human mRNA for KIAA0353 gene partial cds |
| 24572 | >10 | Z38988 | Hs.24192 | ESTs |
| 17810 | >10 | AA151402 | Hs.46531 | H.sapiens mRNA for GCAP-II/uroguanylin precursor |
| 7006 | >10 | Z70295 | Hs.32966 | EST - HG4310-HT4590 |
| 1304 | >10 | HG4310- | Hs.65424 | Tetranectin (plasminogen-binding protein) |
| 5980 | >10 | X64559 | Hs.121713 | Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia) |
| 41987 | >10 | T47059 | Hs.3907 | ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus] |
| 24461 | >10 | W94427 | Hs.89552 | Glutathione S-transferase A2 |
| 2372 | >10 | M16594 | Hs.89552 | Glutathione S-transferase A2 |
| 6001 | >10 | X65727 | Hs.89552 | Glutathione S-transferase A2 |
| 1750 | >10 | L10955 | Hs.93485 | Carbonic anhydrase IV |
| 15130 | >10 | U77643 | Hs.92655 | Human sapiens K12 protein precursor mRNA complete cds |
| 12637 | >10 | AA402656 | Hs.20264 | ESTs |
| 41148 | >10 | R06984 | EST - RC_R06984_3 | ESTs |
| 31652 | >10 | N73950 | Hs.50404 | Human chemokine (TECK) mRNA complete cds |
| 23483 | >10 | T98873 | Hs.143289 | H.sapiens mRNA for metallothionein isoform 1R |
| 4605 | >10 | U51010 | EST - U51010 | EST - U51010 |
| 26359 | >10 | AA509133 | Hs.58115 | ESTs |
| 20856 | >10 | N32506 | Hs.111676 | ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens] |
| 33292 | >10 | W73104 | Hs.89552 | ESTs |
| 12054 | >10 | A3284767 | Hs.21910 | ESTs |
| 41473 | >10 | R48732 | Hs.11006 | ESTs |
| 32568 | >10 | T29246 | Hs.143113 | Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds |
| 6413 | >10 | X87159 | Hs.37129 | Sodium channel nonvoltage-gated 1 beta (Liddle syndrome) |
| 20707 | >10 | N64436 | Hs.28013 | ESTs |
| 27108 | >10 | AA404397 | Hs.58414 | ESTs Highly similar to ENDOTHELIAL ACTIN BINDING PROTEIN [Homo sapiens] |
| 12477 | >10 | AA403032 | Hs.27001 | ESTs |
| 42059 | >10 | T61654 | Hs.93194 | APOLIPROTEIN A1 PRECURSOR |
| 25468 | >10 | AA079072 | Hs.1477 | Insulin-like growth factor binding protein 6 |
| 28910 | >10 | AA303081 | Hs.78253 | ESTs |

FIGURE 6 (CONT.)

| | | | | | |
|-------|-----|----------|----------------|--|---|
| 16938 | >10 | AA059473 | Hs.65783 | ESTs | |
| 14788 | >10 | T03735 | Hs.25885 | ESTs | |
| 7754 | >10 | AA334934 | Hs.75722 | Human NF-IL6-beta protein mRNA complete cds | |
| 6122 | >10 | XT2012 | Hs.75592 | Endoglin (Osler-Render-Weber syndrome 1) | |
| 2848 | >10 | M83286 | Hs.159 | TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR | |
| 23013 | >10 | T16661 | Hs.5725 | ESTs | |
| 19537 | >10 | H30270 | Hs.32583 | ESTs | |
| 4584 | >10 | U50350 | EST - U50350 | EST | |
| 37410 | >10 | AA453552 | Hs.93344 | ESTs | |
| 27959 | >10 | AA464594 | Hs.63392 | ESTs | |
| 35497 | >10 | AA402005 | Hs.141344 | EST | |
| 37013 | >10 | AA443360 | Hs.136238 | ESTs | |
| 39247 | >10 | AA621553 | Hs.112368 | ESTs | ESTs highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens] |
| 13471 | >10 | AA452598 | Hs.109590 | ESTs | |
| 42110 | >10 | T68876 | Hs.76588 | Carboxylesterase 2 (liver) | |
| 10955 | >10 | AA128597 | Hs.18933 | Homo sapiens cGMP-specific phosphodiesterase (PDE3A2) mRNA complete cds | |
| 4918 | >10 | U87733 | Hs.18831 | Human cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE3A2 (PDE3A) mRNA complete cds | |
| 40737 | >10 | N54950 | Hs.81454 | H.sapiens cGMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE3A2 (PDE3A) mRNA complete cds | |
| 30403 | >10 | AA63300 | Hs.110547 | Meis1 (mouse) homolog | |
| 11432 | >10 | AA333369 | Hs.351 | ESTs | |
| 18784 | >10 | F09748 | Hs.7974 | ESTs | |
| 40552 | >10 | U9291 | EST - RC_M6281 | EST | |
| 5773 | >10 | X34162 | Hs.73385 | 84 KD AUTOANTIGEN D1 | |
| 35841 | >10 | AA330566 | Hs.30662 | ESTs | |
| 28858 | >10 | N70065 | Hs.7243 | ESTs | |
| 39729 | >10 | H11469 | Hs.105805 | ESTs | |
| 27387 | >10 | AA426330 | Hs.76284 | ESTs | |
| 39758 | >10 | H15814 | Hs.80455 | Human apM1 mRNA for GSS105 (novel adipose specific collagen like factor) complete cds | |
| 4319 | >10 | U37253 | Hs.59862 | Human microtubule-associated glycoprotein-2 MAGP-2 mRNA complete cds | |
| 2666 | >10 | M59615 | Hs.75562 | Complement component 4A | |
| 41344 | >10 | N39075 | Hs.44534 | EST | |
| 30332 | >10 | R40169 | Hs.6585 | ESTs | |
| 28271 | >10 | AA321200 | Hs.48778 | ESTs | |
| 5834 | >10 | X37129 | Hs.764 | HISTONE H1D | |
| 19048 | >10 | H05464 | Hs.100251 | ESTs | |
| 1429 | >10 | J02854 | Hs.3515 | Human 20-kDa myosin light chain (MLC-2) mRNA complete cds | |
| 19491 | >10 | H27910 | Hs.107384 | ESTs | |
| 29992 | >10 | N26385 | Hs.33064 | Solute carrier family 2 (facilitated glucose transporter) member 5 | |
| 2041 | >10 | L36033 | Hs.77423 | Stromal cell-derived factor 1 | |
| 22855 | >10 | R99509 | Hs.35185 | ESTs | |

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FIGURE 6 (CONT.)

| | | | | | |
|-------|-----|----------|-------------------|--|--|
| 11624 | >10 | AA243954 | Hs.17998 | ESTs | |
| 12512 | >10 | AA405199 | Hs.20733 | ESTs | |
| 14143 | >10 | R45577 | Hs.10683 | ESTs | |
| 5038 | >10 | U77180 | Hs.50002 | Human mRNA for EBF1-1 ligand chemokine complete cds | |
| 5055 | >10 | X59545 | Hs.748 | Basic fibroblast growth factor (bFGF) receptor (shorter form) | |
| 42530 | >10 | W72959 | Hs.74699 | ESTs Weekly similar to SYNAPTOBREVIN 2 [H.sapiens] | |
| 827 | >10 | D87433 | Hs.84753 | Human mRNA for KIAA0246 gene partial cds | |
| 850 | >10 | D78014 | Hs.74556 | Human mRNA for dihydropyrimidinase related protein-3 complete cds | |
| 37350 | >10 | AA452906 | Hs.99289 | EST | |
| 37488 | >10 | AA455178 | Hs.99397 | ESTs | |
| 38546 | >10 | AA431797 | Hs.98763 | EST | |
| 38999 | >10 | AA509007 | EST - RC_AA009007 | | |
| 38191 | >10 | AA487895 | Hs.17311 | ESTs | |
| 8941 | >10 | N27464 | Hs.74670 | Human mRNA for KIAA0146 gene partial cds | |
| 8139 | >10 | AA341723 | Hs.107374 | ESTs | |
| 41522 | >10 | R35966 | Hs.17692 | N-CHILIAIRIN | |
| 35090 | >10 | R09241 | Hs.111301 | Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase) | |
| 41175 | >10 | AA437385 | Hs.115726 | ESTs | |
| 36947 | >10 | U39553 | Hs.70110 | Pigment epithelium-derived factor | |
| 35421 | >10 | AA395686 | Hs.97609 | EST | |
| 4175 | >10 | U39487 | Hs.250 | Xanthine dehydrogenase | |
| 4398 | >10 | AA400272 | Hs.97753 | EST | |
| 35463 | >10 | Z00345 | Hs.127610 | Acyl Coenzyme A dehydrogenase C-2 to C-3 short chain | |
| 7026 | >10 | AA282238 | Hs.118463 | Homo sapiens clone 24519 unknown mRNA partial cds | |
| 34825 | >10 | N24879 | Hs.9063 | ESTs | |
| 20179 | >10 | AA435901 | Hs.59874 | ESTs Weekly similar to p20 protein [R.norvegicus] | |
| 39805 | >10 | W93721 | Hs.23841 | Human mRNA for KIAA0355 gene complete cds | |
| 24447 | >10 | R74386 | Hs.108924 | ESTs | |
| 10247 | >10 | U02388 | Hs.101 | Leukelline B4 omega hydroxylase (cytochrome P450 subfamily IVF) | |
| 3618 | >10 | J03474 | Hs.3157 | SERUM AMYLOID A PROTEIN PRECURSOR | |
| 1464 | >10 | AA055163 | Hs.57975 | Human mRNA for KIAA0355 gene complete cds | |
| 18942 | >10 | AA045300 | Hs.42996 | ESTs | |
| 16736 | >10 | R95580 | Hs.33455 | ESTs | |
| 22958 | >10 | U93358 | Hs.50404 | Human chemokine (TECK) mRNA complete cds | |
| 5248 | >10 | AA135353 | Hs.38022 | ESTs | |
| 7510 | >10 | AA284920 | Hs.13716 | ESTs | |
| 34683 | >10 | H95980 | Hs.12112 | ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus] | |
| 19965 | >10 | N75215 | Hs.43148 | ESTs | |
| 9959 | >10 | AA466185 | Hs.125176 | ESTs | |
| 38136 | >10 | | | | |

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FIGURE 6 (CONT.)

| | | | | |
|-------|-----|----------|-----------|---|
| 36702 | >10 | AA434108 | Hs.101393 | ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens] |
| 3357 | >10 | M99497 | Hs.1915 | PROSTATE-SPECIFIC MEMBRANE ANTIGEN |
| 36763 | >10 | AA435605 | Hs.112095 | EST |
| 4876 | >10 | U66061 | Hs.2049 | Protease serine 2 (trypsin 2) |
| 41149 | >10 | R06986 | Hs.76487 | ESTs |
| 15925 | >10 | Y19492 | Hs.76483 | Homo sapiens mRNA for smoothelin |
| 12944 | >10 | AA428259 | Hs.8769 | ESTs |
| 9317 | >10 | D87468 | Hs.40888 | Human mRNA for KIAA0278 gene partial cds |
| 19331 | >10 | H17865 | Hs.23213 | ESTs |
| 5032 | >10 | U71382 | Hs.90357 | Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds |
| 34239 | >10 | AA335009 | Hs.32245 | ESTs |
| 32852 | >10 | V03006 | Hs.116428 | ESTs |
| 8432 | >10 | X89066 | Hs.34413 | transient receptor potential channel 1 |
| 37001 | >10 | AA443311 | Hs.98996 | ESTs |
| 4500 | >10 | U52101 | Hs.9999 | Human YMP mRNA complete cds |
| 19489 | >10 | P27352 | Hs.287137 | ESTs |
| 23028 | >10 | T17215 | Hs.0652 | ESTs |
| 35359 | >10 | AA339061 | Hs.112661 | ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens] |
| 4655 | >10 | U52959 | Hs.80296 | BRAIN SPECIFIC POLYPEPTIDE PEP-19 |
| 26330 | >10 | AA235984 | Hs.87469 | ESTs |
| 41346 | >10 | RA0395 | Hs.112725 | Lectin-cholesterol acyltransferase |
| 14494 | >10 | AA609845 | Hs.25632 | ESTs Weakly similar to PNG gene [H.sapiens] |
| 4453 | >10 | U43916 | Hs.79368 | Human epithelial membrane protein (CL-20) mRNA complete cds |
| 42758 | >10 | Z41411 | Hs.107040 | ESTs |
| 35637 | >10 | AA402533 | Hs.29283 | ESTs |
| 40392 | >10 | H89587 | Hs.108690 | ESTs |
| 19366 | >10 | H19204 | Hs.133495 | ESTs |
| 5184 | >10 | U62169 | Hs.87234 | Human fizzled homolog (FZD3) mRNA complete cds |
| 869 | >10 | D87468 | Hs.40888 | Human mRNA for KIAA0278 gene partial cds |
| 1595 | >10 | K03207 | Hs.103972 | Salivary proline-rich protein |
| 15574 | >10 | W38778 | Hs.26216 | ESTs |
| 8895 | >10 | C00125 | Hs.24332 | ESTs Weakly similar to similar to deoxyribose-phosphate adolase [C.elegans] |
| 33995 | >10 | AA182845 | Hs.135098 | Homo sapiens FIP2 alternatively translated mRNA complete cds |
| 7949 | >10 | AA283620 | Hs.34956 | ESTs |
| 11670 | >10 | AA32191 | Hs.25199 | Homo sapiens PAC done D1130H16 from 22q12.1-qter |
| 7354 | >10 | AA032348 | Hs.7859 | ESTs |
| 36151 | >10 | AA419011 | Hs.96744 | ESTs |
| 42136 | >10 | T72491 | Hs.73849 | Apolipoprotein C-III |
| 289 | >10 | D16480 | Hs.75960 | Hydroxyacyl-Coenzyme A dehydrogenase/3-ketocacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit |
| 41379 | >10 | RA2223 | Hs.105487 | Homo sapiens mRNA for KIAA0673 protein partial cds |

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FIGURE 6 (CONT.)

| | | | | |
|-------|-----|-----------|--------------|--|
| 34764 | >10 | AA237870 | Hs.1590 | Lymphotoxin-beta |
| 24515 | >10 | Z38289 | Hs.12701 | ESTs |
| 18652 | >10 | Q31111 | Hs.22505 | ESTs |
| 37815 | >10 | AA469552 | Hs.97869 | ESTs |
| 9034 | >10 | C01033 | Hs.29759 | ESTs Weakly similar to IIII ALL SUBFAMILY SX WARNING ENTRY IIII [H.sapiens] |
| 34805 | >10 | AA291522 | Hs.97250 | EST |
| 12246 | >10 | AA3348198 | Hs.14829 | Homo sapiens mRNA for GABA-BR1a (GAB1a) receptor |
| 42153 | >10 | T77723 | Hs.09890 | Pyruvate carboxylase |
| 27110 | >10 | AA404494 | Hs.84112 | CTP synthetase |
| 28331 | >10 | C59722 | Hs.92924 | ESTs |
| 6333 | >10 | X02494 | Hs.2953 | Fibulin 2 |
| 10935 | >10 | AA*121534 | Hs.6823 | ESTs Highly similar to TUBULIN BETA-5 CHAIN [Callus gallus] |
| 27257 | >10 | AA411801 | Hs.45146 | ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens] |
| 3631 | >10 | U03050 | Hs.200 | Homo sapiens C22+ dependent phospholipase A2 mRNA complete cds |
| 4752 | >10 | U59832 | Hs.3947 | Glycoprotein B (Jalaein) beta polypeptide |
| 3766 | >10 | U09570 | Hs.70984 | CYCLOINDEPENDENT KINASE INHIBITOR 1 |
| 4310 | >10 | U37055 | Hs.75034 | Macrophage stimulating 1 (hepatocyte growth factor-like) |
| 26623 | >10 | AA424202 | Hs.55036 | ESTs |
| 5520 | >10 | X08268 | Hs.19218 | Integrin alpha 5 (fibronectin receptor alpha polypeptide) |
| 18720 | >10 | AA444732 | Hs.17208 | ESTs |
| 25336 | >10 | AA353405 | Hs.101404 | ESTs |
| 3547 | >10 | M23069 | Hs.1009 | ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1 |
| 9796 | >10 | M93508 | Hs.73974 | Glutathione S-transferase M2 (muscle) |
| 3206 | >10 | U02979 | Hs.67846 | Human clone HM18 monocytic inhibitory receptor precursor mRNA complete cds |
| 9377 | >10 | H12674 | Hs.5396 | ESTs |
| 41060 | >10 | T33511 | Hs.4844 | ESTs |
| 21911 | >10 | R43960 | Hs.28320 | ESTs |
| 16225 | >10 | AA011305 | Hs.10029 | Calthopain C |
| 18071 | >10 | AA001426 | Hs.40983 | ESTs |
| 25335 | >10 | H68239 | Hs.39122 | ESTs |
| 34986 | >10 | AA344966 | Hs.1285 | Complement component 5 gamma polypeptide |
| 21076 | >10 | N99976 | Hs.8016 | ESTs |
| 4402 | >10 | U41518 | Hs.74602 | AQUAPORIN-CHIP |
| 20423 | >10 | M49308 | Hs.104938 | ESTs |
| 18575 | >10 | AA031948 | Hs.57548 | ESTs |
| 28264 | >10 | AA521060 | Hs.48765 | ESTs |
| 9003 | >10 | C00803 | Hs.107882 | ESTs |
| 5632 | >10 | X15357 | EST - X15357 | EST |
| 20852 | >10 | N69540 | Hs.17713 | ESTs |
| 34585 | >10 | AA281002 | Hs.40735 | ESTs |

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FIGURE 6 (CONT.)

| | | | | | |
|-------|-----|----------|---------------------|--|--|
| 33590 | >10 | Z36607 | Hs.62248 | ESTs | |
| 8904 | >10 | AF002256 | Hs.95180 | Homo sapiens killer cell receptor (KIR103) mRNA, allele ASD1 complete cds | |
| 3307 | >10 | M9809 | Hs.89578 | BASIC TRANSCRIPTION FACTOR 62 KO SUBUNIT | |
| 39200 | >10 | AA621246 | Hs.112956 | EST | |
| 24712 | >10 | Z36652 | Hs.27457 | ESTs | |
| 2199 | >10 | LA9169 | Hs.76578 | Human GUS3 mRNA complete cds | |
| 38642 | >10 | AA508646 | Hs.94970 | Human mRNA for KIAA0005 gene partial cds | |
| 41628 | >10 | R70212 | Hs.79630 | Immunoglobulin-associated alpha | |
| 6834 | >10 | Z18054 | Hs.2990 | S100 calcium-binding protein, AS (formerly S100D) | |
| 40662 | >10 | N38212 | Hs.107197 | ESTs | |
| 37333 | >10 | AA432158 | Hs.75122 | TRANSFORMING PROTEIN RHOB | |
| 3592 | >10 | U19713 | Hs.75384 | Allograft inflammatory factor 1 | |
| 36734 | >10 | AA608792 | Hs.112591 | EST | |
| 37836 | >10 | AA470135 | Hs.112238 | ESTs | |
| 10000 | >10 | N79674 | Hs.75915 | ESTs | |
| 30658 | >10 | N11105 | Hs.111223 | ESTs | |
| 17629 | >10 | AA131919 | Hs.69009 | ESTs | |
| 36290 | >10 | AA423870 | Hs.98378 | ESTs | |
| 24122 | >10 | W46947 | Hs.41188 | ESTs | |
| 1066 | >10 | HG2705- | EST - HG2705-HT2801 | | |
| 12389 | >10 | AA395633 | Hs.24872 | ESTs | |
| 26025 | >10 | AA235874 | Hs.88888 | PUTATIVE DNA BINDING PROTEIN A20 | |
| 41104 | >10 | R01388 | EST - RC_R01388 | | |
| 33566 | >10 | W93015 | Hs.73166 | Treacher Collins syndrome susceptibility protein | |
| 23379 | >10 | AA058693 | Hs.111941 | Human adenyllyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds | |
| 17807 | >10 | AA160530 | Hs.72447 | ESTs | |
| 38838 | >10 | AA436163 | Hs.95851 | Homo sapiens Pig12 (PIG12) mRNA complete cds | |
| 19524 | >10 | H29566 | Hs.63466 | Homo sapiens clone 23579 mRNA sequence | |
| 21834 | >10 | R44449 | Hs.48778 | ESTs | |
| 32456 | >10 | T15929 | Hs.65264 | ESTs | |
| 15440 | >10 | W27301 | Hs.111652 | ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonaspora curvula] | |
| 2807 | >10 | M55210 | Hs.87428 | Laminin gamma 1 (formerly LAMB2) | |
| 34193 | >10 | AA232251 | Hs.128630 | ESTs | |
| 14584 | >10 | AA621414 | Hs.110903 | Homo sapiens transmembrane protein mRNA complete cds | |
| 38752 | >10 | AA508652 | Hs.112903 | EST | |
| 5294 | >10 | U50065 | Hs.79351 | Human two P-domain K+ channel TWIK-1 mRNA complete cds | |
| 84 | >10 | AF001369 | EST - AF001369.J | | |
| 4856 | >10 | U64603 | Hs.82071 | Human msj related gene 1 (msj) mRNA complete cds | |
| 13974 | >10 | AA479289 | Hs.21107 | ESTs | |
| 26151 | >10 | AA250088 | Hs.105509 | ESTs | |

FIGURE 6 (CONT.)

| | | | | |
|-------|-----|----------|-----------|--|
| 5938 | >10 | X62535 | Hs.74044 | Diacetyl glycerol kinase alpha (BOKD) |
| 17717 | >10 | AA138541 | Hs.71647 | EST |
| 12404 | >10 | AA400262 | Hs.23766 | ESTs |
| 2407 | >10 | M19373 | Hs.50788 | GRANZYME A PRECURSOR |
| 26920 | 10 | AA220413 | Hs.65943 | Spleen focus forming virus (SFFV) proviral integration oncogene sp1 |
| 37675 | 10 | AA460377 | Hs.98616 | ESTs |
| 41827 | 10 | T15445 | Hs.94941 | H-sapiens mRNA for F2583.3 kinase like protein from C.elegans |
| 82 | 10 | AF003959 | Hs.110903 | Homo sapiens transmembrane protein mRNA complete cds |
| 203 | 10 | D12620 | Hs.106242 | CYTTOCHROME P450 1V3 |
| 24159 | 10 | W57862 | Hs.21289 | ESTs |
| 5302 | 10 | U80043 | Hs.73041 | Human butyrophilin (BTF1) mRNA complete cds |
| 2219 | 10 | L76670 | Hs.109510 | Homo sapiens nlat7 mRNA complete cds |
| 24392 | 10 | W69566 | Hs.59589 | Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds |
| 38159 | 10 | AA419279 | Hs.82613 | Colony-stimulating factor 1 (M-CSF) |
| 28251 | 10 | AA504512 | Hs.78652 | ESTs Weakly similar to ZK792.1 [C.elegans] |
| 37592 | 10 | AA458968 | Hs.93990 | ESTs |
| 39619 | 9 | F10640 | Hs.12354 | ESTs |
| 8240 | 9 | AA397841 | Hs.106679 | ESTs |
| 10987 | 9 | AA101632 | Hs.22971 | ESTs |
| 37530 | 9 | AA455474 | Hs.100330 | ESTs |
| 42850 | 9 | W92272 | Hs.25801 | Homo sapiens zinc finger helicase (hZF) mRNA complete cds |
| 9011 | 9 | C01394 | Hs.106623 | Homo sapiens clone 24818 mRNA sequence |
| 3490 | 9 | S77763 | Hs.75543 | Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds |
| 36691 | 9 | AA432391 | Hs.57357 | ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H-sapiens] |
| 3478 | 9 | S76992 | Hs.104005 | Vav 2 oncogene |
| 42034 | 9 | T56281 | Hs.110440 | Human metallothionein (MT)-I gene |
| 11845 | 9 | AA259094 | Hs.10639 | ESTs Weakly similar to unknown [S.cerevisiae] |
| 19317 | 9 | H17476 | Hs.11615 | ESTs Weakly similar to dual-specificity phosphatase [H-sapiens] |
| 42395 | 8 | W42733 | Hs.109570 | ESTs |
| 11425 | 8 | AA233267 | Hs.25511 | Homo sapiens mRNA for Hic-5 partial cds |
| 15310 | 8 | W19098 | Hs.7921 | ESTs |
| 36601 | 8 | AA431337 | Hs.98017 | ESTs |
| 13469 | 8 | AA453456 | Hs.7301 | ESTs |
| 37514 | 8 | AA455914 | Hs.1019 | Pseudogenized hormone receptor 1 |
| 5968 | 8 | X85644 | Hs.7593 | HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2 |
| 33959 | 8 | U83074 | Hs.93342 | ESTs |
| 4901 | 8 | X55446 | Hs.3116 | H-sapiens mRNA for 2.19 gene |
| 11129 | 8 | AA158973 | Hs.15970 | ESTs |
| 31997 | 8 | N64551 | Hs.50660 | ESTs |
| 40438 | 8 | N21694 | Hs.30590 | Human mRNA for KIAA0061 gene partial cds |

FIGURE 6 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|--|
| 34471 | 8 | AA259843 | Hs.111376 | ESTs | |
| 25530 | 8 | AA098934 | Hs.83428 | Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p103) | |
| 30471 | 7 | D02605 | Hs.107894 | ESTs | |
| 25100 | 7 | AA019426 | Hs.103343 | EST | |
| 15915 | 7 | Y08888 | Hs.82577 | Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog) (PROTEIN DXF34) hypothetical protein E | |
| 19097 | 7 | H08171 | Hs.30842 | ESTs | |
| 35353 | 7 | AA398062 | Hs.97699 | ESTs | |
| 36822 | 7 | AA459578 | Hs.98852 | EST | |
| 36959 | 7 | AA400893 | Hs.41717 | Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds | |
| 1978 | 7 | U11447 | Hs.101815 | Human Rat guanine nucleotide dissociation stimulator mRNA (ratil) cds | |
| 26178 | 7 | L29339 | Hs.1964 | Solute carrier family 5 (sodium/glucose cotransporter) member 1 | |
| 36428 | 7 | AA231153 | Hs.27910 | Human sapiens centronomal NaH2-activated protein 1 (C-NAP1) mRNA complete cds | |
| 26333 | 7 | AA247003 | Hs.95551 | Human Cardiac myosin binding protein-C (MyBP-C) gene complete cds | |
| 40387 | 7 | H54660 | Hs.62280 | ESTs | |
| 27236 | 7 | AA417037 | Hs.108873 | ESTs | |
| 20083 | 7 | H86679 | Hs.67805 | ESTs | |
| 21561 | 7 | R3245 | Hs.28029 | ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus] | |
| 21223 | 7 | AA450118 | Hs.23076 | ESTs | |
| 34845 | 7 | AA593420 | Hs.110130 | Human sapiens chromosome 19 cosmid F2329 | |
| 15059 | 7 | U53831 | Hs.25722 | ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens] | |
| 1945 | 7 | L25878 | Hs.85280 | ESTs Moderately similar to transcription enhancer factor 1 (TEF1) [H. sapiens] | |
| 42848 | 7 | W92150 | Hs.89549 | Human Interferon regulatory factor 7 (hunnif7) mRNA complete cds | |
| 20041 | 7 | H87012 | Hs.79310 | Epoxide hydrolase 1 microsomal (xenobiotic) | |
| 7053 | 6 | Z94721 | Hs.11050 | Human GAP SH3 binding protein mRNA complete cds | |
| 23843 | 6 | T92561 | Hs.75792 | ESTs Weakly similar to L8004.7 gene product [S. cerevisiae] | |
| 22815 | 6 | AA149889 | Hs.110422 | ESTs | |
| 8473 | 6 | AA337346 | Hs.99200 | ESTs Weakly similar to A-kinase anchor protein B5 AKAP95 [R. norvegicus] | |
| 34618 | 6 | AA382143 | Hs.2967 | SHB adaptor protein (a Src homology 2 protein) | |
| 11074 | 6 | AA148983 | Hs.58034 | H. sapiens mRNA for melanoma growth regulatory protein M1A | |
| 17533 | 6 | AA127098 | Hs.23068 | ESTs | |
| 28973 | 6 | F04014 | Hs.71057 | EST | |
| 17042 | 6 | AA070397 | Hs.65996 | ESTs | |
| 15246 | 8 | W01084 | Hs.94628 | EST - RC_AA070397 | |
| 2247 | 8 | M10321 | Hs.110802 | VON WILLEBRAND FACTOR PRECURSOR | |
| 30810 | 8 | N53419 | Hs.47846 | ESTs | |
| 13348 | 8 | AA446267 | Hs.17914 | ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA SUBUNIT [M. musculus] | |
| 1789 | 6 | L13258 | Hs.936 | Solute carrier family 17 (sodium phosphate) member 2 | |
| 16627 | 5 | AA036779 | Hs.61826 | Human sapiens clone 23828 mRNA sequence | |

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FIGURE 6 (CONT.)

| | | | | |
|-------|---|----------|-----------------------|---|
| 27103 | 5 | AA04282 | Hs.63481 | ESTs Weakly similar to kynurenine/alpha-aminoadipate aminotransferase [R norvegicus] |
| 12631 | 5 | AA41293 | Hs.21258 | ESTs |
| 11599 | 5 | AA24269 | Hs.7508 | ESTs |
| 9010 | 5 | C01360 | Hs.67354 | Homo sapiens clone 23504 mRNA sequence |
| 4660 | 5 | US3225 | Hs.75263 | Spring pekin 1 |
| 5244 | 5 | U85922 | Hs.87197 | Human clone IMAGE35527, unknown protein mRNA partial cds |
| 7853 | 5 | AA36403 | Hs.74750 | Homo sapiens mRNA for KIAA0554, protein partial cds |
| 27617 | 5 | AA44614 | Hs.55409 | ESTs |
| 38400 | 5 | D65419 | Hs.81915 | STATHMIN |
| 37329 | 5 | AA45612 | Hs.99410 | ESTs |
| 11658 | 5 | AA26236 | Hs.106385 | ESTs |
| 37294 | 5 | AA450127 | Hs.110571 | ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus] |
| 23201 | 5 | T40652 | Hs.8279 | ESTs |
| 28767 | 5 | D45008 | Hs.83792 | Surfactant pulmonary-associated protein D |
| 3151 | 4 | M63652 | Hs.53155 | Properdin P factor complement |
| 23196 | 4 | H24455 | Hs.85053 | Homo sapiens clone 24440 mRNA sequence |
| 12663 | 4 | AA425762 | Hs.27973 | ESTs |
| 42486 | 4 | W08410 | Hs.106857 | Calbindin 2 (28K calsectin) |
| 23571 | 4 | T80529 | Hs.108169 | ESTs |
| 12376 | 4 | AA339271 | Hs.13610 | ESTs |
| 27694 | 4 | AA460319 | Hs.49469 | ESTs |
| 24935 | 4 | AFX- | AFX-HUMGAPDHIM33197_M | |
| 4238 | 4 | U33053 | Hs.2499 | Human lipid-activated protein kinase PRK1 mRNA complete cds |
| 41844 | 4 | T15833 | Hs.100227 | EST |
| 20111 | 4 | N21380 | Hs.25497 | H.sapiens mRNA for ROX protein |
| 8316 | 4 | AA410529 | Hs.30732 | ESTs |
| 39754 | 4 | H21819 | Hs.14896 | Homo sapiens clone 24550 mRNA sequence |
| 1517 | 4 | J04501 | Hs.772 | Glycogen synthase 1 (muscle) |
| 9164 | 4 | D38081 | Hs.69867 | Thromboxane A2 receptor |
| 35027 | 4 | AA349596 | Hs.96937 | ESTs |
| 14156 | 4 | AA490182 | Hs.116596 | ESTs |
| 41950 | 4 | T33137 | Hs.7967 | ESTs |
| 34360 | 4 | AA251547 | Hs.104358 | EST |
| 34360 | 4 | X35808 | Hs.9568 | Human mRNA for KIAA0385 gene complete cds |
| 6547 | 4 | N69980 | Hs.19167 | ESTs |
| 20963 | 4 | AA419200 | Hs.5737 | ESTs |
| 12734 | 4 | D80154 | Hs.55340 | ESTs |
| 39497 | 4 | K03474 | EST - K03474 | |
| 1680 | 4 | AA408231 | Hs.100113 | Human mRNA for KIAA0381 gene partial cds |
| 27146 | 4 | AA057620 | Hs.30607 | ESTs |
| 10763 | 4 | | | |

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FIGURE 6 (CONT.)

| | | | | | |
|-------|---|----------|--------------|--|--|
| 17007 | 4 | AA069666 | Hs.67317 | ESTs | |
| 18322 | 4 | AA454115 | Hs.6000 | ESTs | |
| 18444 | 4 | AA232546 | Hs.68061 | ESTs | |
| 27655 | 3 | AA447769 | Hs.134724 | ESTs | |
| 21382 | 3 | RV6886 | Hs.88616 | PROTEIN KINASE C THETA TYPE | |
| 2052 | 3 | L35816 | Hs.75329 | Inactivated polyphosphate phosphatase-like protein 1 (SIC protein) | |
| 9339 | 3 | C02049 | Hs.102291 | ESTs | |
| 34888 | 3 | AA030378 | Hs.94479 | Human GT334 protein (GT334) gene mRNA, complete cds | |
| 11047 | 3 | AA142549 | Hs.22660 | ESTs | |
| 19451 | 3 | H23747 | Hs.31697 | ESTs | |
| 2822 | 3 | M55621 | Hs.117946 | N-acetylglucosaminyltransferase I | |
| 13828 | 3 | AA478441 | Hs.11590 | ESTs | |
| 12054 | 3 | AA283848 | Hs.11367 | ESTs Weakly similar to KIAA0009 [H.sapiens] | |
| 3836 | 3 | U12707 | Hs.2157 | Wiskott-Aldrich syndrome (eczema-thrombocytopenia) | |
| 4528 | 3 | U48251 | Hs.7871 | Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds | |
| 42054 | 3 | T63364 | Hs.9225 | ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimentalis] | |
| 4596 | 3 | U60743 | Hs.19520 | Sodiumpotassium ATPase gamma subunit | |
| 4914 | 3 | U67611 | EST - U67611 | | |
| 20168 | 3 | N24106 | Hs.2799 | Cartilage linking protein 1 | |
| 24281 | 3 | W79773 | Hs.18511 | ESTs | |
| 19634 | 3 | H44866 | Hs.31597 | ESTs | |
| 10989 | 3 | AA132266 | Hs.8023 | Homo sapiens mRNA for SPQF | |
| 6587 | 3 | X97748 | EST - X97748 | | |
| 14096 | 3 | AA487558 | Hs.8135 | ESTs | |
| 13350 | 3 | AA448297 | Hs.8944 | ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens] | |
| 33930 | 3 | AA165539 | Hs.95570 | ESTs | |
| 34215 | 3 | AA233655 | Hs.104252 | UTROPHIN | |
| 22569 | 3 | R71393 | Hs.29190 | ESTs | |
| 20065 | 3 | H86557 | Hs.27291 | ESTs | |
| 31091 | 3 | N50376 | Hs.138746 | EST | |
| 2453 | 3 | M22519 | Hs.73385 | MYOSIN LIGHT CHAIN ALKALINE SMOOTH-MUSCLE ISOFORM | |
| 28913 | 3 | F01560 | Hs.25853 | ESTs Highly similar to co-repressor protein [M.musculus] | |
| 14323 | 3 | AA598575 | Hs.12851 | ESTs | |
| 34914 | 3 | AA338729 | Hs.130306 | ESTs | |
| 34914 | 3 | AA496891 | Hs.5011 | ESTs Weakly similar to The hsa127 gene product is related to S. pombe rad21 gene product [H.sapiens] | |
| 14230 | 3 | Z38804 | Hs.24355 | ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus] | |
| 24594 | 3 | R79560 | Hs.28674 | ESTs | |
| 22569 | 3 | R32143 | Hs.28694 | ESTs | |
| 21156 | 3 | AA021284 | Hs.02554 | ESTs Moderately similar to sodium-calcium exchanger form 3 [R.noregicus] | |
| 16404 | 3 | H95942 | Hs.88729 | ESTs | |
| 23310 | 3 | | | | |

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FIGURE 6 (CONT.)

| | | | | |
|-------|---|----------|---------------------|--|
| 9758 | 3 | M25393 | Hs.127610 | Aoy-Coenzyme A dehydrogenase C2 to C3 short chain |
| 9806 | 2 | M79462 | Hs.89633 | Probable transcription factor PML (alternative products) |
| 19259 | 2 | H16568 | Hs.23748 | ESTs |
| 34031 | 2 | AA192614 | Hs.83577 | Human LIM protein MLP mRNA complete cds |
| 33259 | 2 | M73790 | Hs.73803 | IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR |
| 3276 | 2 | M93718 | Hs.75963 | Nitric oxide synthase 3 (endothelial cell) |
| 31704 | 2 | M75055 | Hs.14632 | ESTs |
| 10310 | 2 | R67373 | Hs.75429 | ESTs |
| 22388 | 2 | R63695 | Hs.1432 | Protein kinase C substrate 80K-H |
| 20938 | 2 | M73988 | Hs.37477 | ESTs Weakly similar to No definition line [C.elegans] |
| 5935 | 2 | X62466 | Hs.103338 | CDW52 antigen (CAMPATH-1 antigen) |
| 41495 | 2 | R49689 | Hs.5290 | ESTs Weakly similar to C05G8.3 [C.elegans] |
| 25403 | 2 | AA053316 | EST - RC_AA053316 | EST - RC_AA053316 |
| 27965 | 2 | AA462657 | Hs.24912 | Homo sapiens bicucullin (BICD) mRNA complete cds |
| 40632 | 2 | N45221 | EST - RC_N45221 | EST - RC_N45221 |
| 15527 | 2 | W09768 | Hs.63260 | Phosphodiesterase 8A cGMP-specific rod alpha |
| 31672 | 2 | N74398 | Hs.91681 | ESTs |
| 984 | 2 | HG1804L | EST - HG1804L-1029 | EST - HG1804L-1029 |
| 12439 | 2 | AA401452 | Hs.32050 | ESTs |
| 24223 | 2 | W70189 | Hs.26696 | ESTs |
| 21052 | 2 | N93764 | Hs.10175 | ESTs Weakly similar to hypothetical protein [H.sapiens] |
| 34140 | 2 | AA215537 | Hs.104168 | ESTs |
| 5130 | 2 | U73268 | Hs.65053 | Homo sapiens clone 24440 mRNA sequence |
| 30041 | 2 | N27628 | Hs.132744 | Homo sapiens clone 24525 mRNA sequence |
| 19202 | 2 | H11509 | Hs.22462 | ESTs |
| 41350 | 2 | R40442 | Hs.75552 | Guanylate S-transferase M5 |
| 914 | 2 | HG1019L | EST - HG1019-HT1019 | EST - HG1019-HT1019 |
| 31958 | 2 | N93495 | Hs.54950 | ESTs |
| 12014 | 2 | AA261769 | Hs.7214 | Human Hsp70 (HSP70) mRNA complete cds |
| 39777 | 2 | H18412 | Hs.75553 | Human clone ID 193225 NAO (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds |
| 19147 | 2 | H03751 | Hs.117619 | ESTs |
| 11199 | 2 | AA176446 | Hs.10024 | ESTs |
| 8477 | 2 | X91504 | Hs.64904 | Transcription factor COUP 2 (a.k.a. ARP1) |
| 16336 | 2 | AA019601 | Hs.75949 | EXTRACELLULAR SIGNAL-REGULATED KINASE 3 |
| 24058 | 2 | W23769 | Hs.109047 | ESTs |
| 26180 | 2 | AA251230 | Hs.112272 | ESTs |
| 37177 | 2 | AA447968 | Hs.7765 | ESTs |
| 41984 | 2 | T47601 | Hs.138605 | ESTs |
| 36532 | 2 | AA429659 | Hs.69882 | Acrosin |
| 1450 | 2 | J03071 | Hs.115352 | Growth hormone 1 |

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FIGURE 6 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|--|
| 24819 | 2 | Z40923 | Hs.24812 | ESTs | |
| 6932 | 2 | X95325 | Hs.89491 | DNA-BINDING PROTEIN A | |
| 27085 | 2 | AA402486 | Hs.77978 | ESTs | |
| 20487 | 2 | NS2322 | Hs.19978 | ESTs | |
| 724 | 2 | D83703 | Hs.30729 | Peroxisomal biogenesis factor 6 | |
| 4132 | 2 | U27655 | Hs.62284 | Human ROP3 mRNA complete cds | |
| 13875 | 2 | AA449716 | Hs.5723 | ESTs | |
| 13908 | 2 | AA460045 | Hs.7934 | ESTs | |
| 22306 | 2 | R39906 | Hs.100530 | ESTs | |
| 23167 | 2 | T33164 | Hs.12640 | Human sapiens germline mRNA sequence | |
| 11320 | 2 | AA213567 | Hs.22222 | ESTs | |
| 24608 | 2 | Z38888 | Hs.25046 | ESTs | |
| 13163 | 2 | AA437225 | Hs.22410 | ESTs | |
| 1139 | 2 | HG3327- | | EST - HG3327-HT3404 | |
| 35572 | 2 | AA401489 | | EST - RC_AA401489 | |
| 6964 | 2 | Z49105 | | H.sapiens HD21 mRNA | |
| 30963 | 2 | N59373 | Hs.137591 | ESTs | |
| 16164 | 2 | AA007509 | Hs.28812 | Hs.75395 Human mRNA for TPRD complete cds | |
| 2174 | 2 | L42611 | Hs.75395 | ESTs | |
| 38958 | 2 | AA609707 | Hs.111758 | KERATIN TYPE II CYTOSKELETAL 6D | |
| 37919 | 2 | AA478162 | Hs.112751 | ESTs | |
| 28605 | 2 | D81123 | Hs.104965 | ESTs | |
| 19545 | 2 | U09117 | Hs.57475 | ESTs | |
| 3745 | 2 | H37834 | Hs.80776 | Human phospholipase c delta 1 mRNA complete cds | |
| 8416 | 2 | AA428531 | Hs.32659 | EST - AA428531 | |
| 17569 | 2 | AA128926 | | EST - RC_AA128926 | |
| 19354 | 2 | H18029 | Hs.121515 | ESTs | |
| 7598 | 2 | AA174185 | Hs.3354 | Human sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds | |
| 25395 | 2 | AA059099 | Hs.109727 | ESTs | |
| 14176 | 2 | AA430620 | Hs.11679 | ESTs | |
| 29487 | 2 | H85120 | Hs.60881 | N-ACETYL-LACTOSAMINE SYNTHASE | |
| 10197 | 2 | R84169 | Hs.50785 | Human sapiens vesicle trafficking protein sec22b mRNA complete cds | |
| 19488 | 2 | H27575 | Hs.25604 | ESTs | |
| 10588 | 2 | AA029703 | Hs.36574 | ESTs | |
| 30799 | 2 | NS3143 | Hs.64001 | ESTs | |
| 9536 | 2 | LQ7882 | Hs.108415 | Human peroxisome proliferator activated receptor mRNA complete cds | |
| 27185 | 2 | AA414173 | Hs.65311 | ESTs | |
| 17438 | 2 | AA115508 | Hs.2760 | Jun D proto-oncogene | |
| 24832 | 2 | AFFX- | | AFFX-HSAC07X00351_M | |
| 10944 | 2 | AA129569 | | ESTs Weakly similar to F56G12.9 [C.elegans] | |

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FIGURE 6 (CONT.)

| | | | | |
|-------|---|----------|----------------------|--|
| 4324 | 2 | T98199 | Hs.142702 | ESTs |
| 34756 | 2 | A4207655 | Hs.0245 | ESTs |
| 12743 | 2 | AA421050 | Hs.24545 | ESTs |
| 13676 | 2 | AA493989 | Hs.26350 | Homo sapiens mRNA for tyrosyl sulfoxidase-2 |
| 13069 | 2 | AA430474 | Hs.19466 | ESTs |
| 7403 | 2 | AA094921 | Hs.79788 | ESTs |
| 35659 | 2 | AA404707 | Hs.54865 | ESTs |
| 17701 | 2 | AA135941 | Hs.71626 | ESTs |
| 18713 | 2 | F04686 | Hs.21782 | ESTs |
| 8314 | 2 | AA103355 | Hs.103081 | ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens] |
| 7990 | 2 | AA291766 | Hs.32822 | ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens] |
| 42791 | 2 | AFFX- | AFFX-HUMGAPDH33197_M | |
| 6893 | 1 | Z30543 | Hs.123123 | H.sapiens mRNA for chloride channel (putative) 2138bp |
| 35607 | 1 | AA402267 | Hs.133475 | ESTs Weakly similar to zinc finger protein [H.sapiens] |
| 9468 | 1 | H46074 | Hs.31562 | ESTs |
| 29469 | 1 | H62929 | EST - RC_H62929 | EST - RC_H62929 |
| 18692 | 1 | F04444 | Hs.6217 | ESTs |
| 33205 | 1 | AA398161 | Hs.97602 | ESTs |
| 22184 | 1 | R53520 | Hs.102755 | ESTs |
| 28815 | 1 | D65267 | Hs.56782 | ESTs |
| 17813 | 1 | AA151480 | Hs.91202 | ESTs |
| 24655 | 1 | Z38191 | Hs.27792 | ESTs Weakly similar to LphT1p [S.cerevisiae] |
| 15611 | 1 | W51743 | Hs.35096 | ESTs |
| 15700 | 1 | W73959 | Hs.78061 | Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds |
| 36770 | 1 | AA433753 | EST - RC_AA433753 | EST - RC_AA433753 |
| 32400 | 1 | R97176 | Hs.110783 | ESTs |
| 10802 | 1 | AA059425 | Hs.20573 | ESTs |
| 17583 | 1 | AA128856 | EST - RC_AA128856 | EST - RC_AA128856 |
| 20268 | 1 | X32118 | Hs.107365 | ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens] |
| 14447 | 1 | AA068945 | Hs.11759 | ESTs |
| 12652 | 1 | AA428521 | Hs.18528 | Homo sapiens mRNA for NA14 protein |
| 19738 | 1 | H53059 | Hs.15546 | ESTs |
| 14471 | 1 | AA600346 | Hs.20102 | ESTs |
| 5796 | 1 | X55019 | Hs.59975 | Cholelergic nicotinic delta polypeptide |
| 18441 | 1 | AA232508 | Hs.77490 | ESTs |
| 10164 | 1 | RS4743 | Hs.19400 | ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae] |
| 8630 | 1 | AB002319 | Hs.8663 | Human mRNA for KIAA0321 gene partial cds |
| 8692 | 1 | AA477691 | Hs.104476 | ESTs |
| 35620 | 1 | AA402493 | Hs.10552 | ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus] |
| 35401 | 1 | AA398593 | Hs.97882 | EST |

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FIGURE 6 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|--|
| 10901 | 1 | AA112307 | Hs.25224 | ESTs | |
| 19546 | 1 | H37501 | Hs.32706 | ESTs | |
| 30232 | 1 | N35978 | Hs.82264 | ESTs | |
| 39087 | 1 | AA620607 | Hs.111591 | ESTs | |
| 37896 | 1 | AA474743 | Hs.77039 | Ribosomal protein S28 | |
| 41552 | 1 | R59352 | Hs.101253 | Human mRNA for KIAA0296 gene complete cds | |
| 11467 | 1 | AA234089 | Hs.14593 | ESTs | |
| 8215 | 1 | AA389673 | Hs.84344 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 15505 | 1 | W28366 | Hs.7252 | Homo sapiens clone 24800 mRNA sequence | |
| 9634 | 1 | M82299 | Hs.22554 | Homo sapiens clone 24800 mRNA sequence | |
| 0159 | 1 | D31483 | Hs.90062 | Homo sapiens clone 23955 unknown mRNA partial cds | |
| 42218 | 1 | T86444 | Hs.110095 | ESTs | |
| 15526 | 1 | W28790 | Hs.8124 | ESTs | |
| 17790 | 1 | AA150182 | Hs.42262 | ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans] | |
| 9777 | 1 | M57583 | Hs.95946 | GRANZYME H PRECURSOR | |
| 15373 | 1 | W26376 | Hs.74563 | THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR | |
| 12076 | 1 | AA284362 | Hs.5448 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 15391 | 1 | V26691 | Hs.15951 | ESTs | |
| 12905 | 1 | AA427537 | Hs.32419 | ESTs | |
| 39820 | 1 | H24085 | Hs.25443 | ESTs | |
| 13109 | 1 | AA435838 | Hs.7985 | ESTs | |
| 24249 | 1 | W73069 | Hs.12900 | ESTs | |
| 16514 | 1 | AA027946 | Hs.46098 | ESTs | |
| 16797 | 1 | AA046860 | Hs.40342 | ESTs | |
| 15351 | 1 | V23496 | Hs.107725 | ESTs Weakly similar to LIS-1 protein [H.sapiens] | |
| 11680 | 1 | AA352762 | Hs.31235 | ESTs | |
| 22699 | 1 | T16510 | Hs.6624 | ESTs | |
| 24490 | 1 | Z38153 | Hs.26921 | ESTs | |
| 24368 | 1 | W87280 | Hs.124000 | ESTs | |
| 22595 | 1 | R77631 | Hs.29126 | ESTs | |
| 15358 | 1 | W26105 | Hs.5961 | ESTs | |
| 24196 | 1 | W61319 | Hs.37462 | ESTs Highly similar to COTOMER ZETA SUBUNIT [Bos taurus] | |
| 22272 | 1 | R59522 | Hs.26590 | ESTs | |
| 16134 | 1 | AA024494 | Hs.61199 | ESTs | |
| 22692 | 1 | R88711 | Hs.34193 | ESTs | |
| 38830 | 1 | AA509189 | Hs.116415 | ESTs | |
| 42547 | 1 | W73946 | | EST - RC_W73946 | |
| 34885 | 1 | AA302831 | Hs.57732 | Homo sapiens p30eta2 MAP kinase mRNA complete cds | |
| 18445 | 1 | AA232648 | Hs.87068 | ESTs | |
| 18070 | 1 | AA180352 | Hs.72733 | ESTs | |

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FIGURE 6 (CONT.)

23923 1 T96407 Hs.17B12 ESTs

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FIGURE 7

| Primary Key | fold downregulated of Tumor vs | Accession | Unigene CLUSTER | Unigene Descriptor |
|-------------|--------------------------------|-----------|-------------------|--|
| 2348 | >10 | M15666 | Hs.75592 | Adolase B nucleoside-bisphosphate |
| 6463 | >10 | X90908 | Hs.74126 | H.sapiens mRNA for I-15P (I-BABP) protein |
| 42139 | >10 | T73335 | Hs.63194 | APOLIPOPROTEIN A-I PRECURSOR |
| 4544 | >10 | U48959 | Hs.75550 | H.sapiens mRNA for myosin light chain kinase |
| 1583 | >10 | K02765 | Hs.89512 | COMPLEMENT C3 PRECURSOR |
| 2426 | >10 | M19828 | Hs.585 | Apolipoprotein B (including Ag(a) antigen) |
| 8859 | >10 | AB002351 | Hs.10587 | Human mRNA for KIAA0353 gene partial cds |
| 24572 | >10 | Z38686 | Hs.24192 | ESTs |
| 17810 | >10 | AA151402 | Hs.46531 | ESTs |
| 7008 | >10 | Z70295 | Hs.32966 | H.sapiens mRNA for GCAP-III/retinoylamin precursor |
| 1304 | >10 | HG43170 | Hs.45310 | EST - HG4310-HT4590 |
| 5980 | >10 | X84559 | Hs.65424 | Tetranectin (plasminogen-binding protein) |
| 11987 | >10 | T47089 | Hs.121713 | Cytocrome P450 subfamily XX (steroid 21-hydroxylase congenital adrenal hyperplasia) |
| 24461 | >10 | V94227 | Hs.3807 | ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus] |
| 2372 | >10 | M16594 | Hs.89552 | Glutathione S-transferase A2 |
| 6001 | >10 | X65727 | Hs.89552 | Glutathione S-transferase A2 |
| 1750 | >10 | L10935 | Hs.68465 | Carbonic anhydrase IV |
| 15130 | >10 | U77043 | Hs.35855 | Human sapiens K12 protein precursor mRNA complete cds |
| 12467 | >10 | AA402656 | Hs.26264 | ESTs |
| 41146 | >10 | R08964 | EST - RC_R06964_s | ESTs |
| 31852 | >10 | N73958 | Hs.50404 | Human chemokine (TECK) mRNA complete cds |
| 23483 | >10 | T68873 | Hs.143289 | H.sapiens mRNA for metallothionein isoform 1R |
| 4605 | >10 | U51010 | EST - U51010 | ESTs |
| 26359 | >10 | AA609133 | Hs.58115 | ESTs |
| 24066 | >10 | V32506 | Hs.111676 | ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens] |
| 32262 | >10 | W73194 | Hs.80952 | ESTs |
| 12084 | >10 | AA284767 | Hs.21910 | ESTs |
| 41473 | >10 | R48732 | Hs.11006 | ESTs |
| 32568 | >10 | T25248 | Hs.143113 | Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds |
| 6413 | >10 | X87159 | Hs.37129 | Sodium channel nonvoltage-gated 1 beta (Liddle syndrome) |
| 2707 | >10 | N64436 | Hs.20913 | ESTs |
| 20707 | >10 | AA404367 | Hs.59414 | ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens] |
| 27108 | >10 | AA403032 | Hs.21701 | ESTs |
| 42059 | >10 | T61654 | Hs.93194 | APOLIPOPROTEIN A-I PRECURSOR |
| 25468 | >10 | AA079072 | Hs.1477 | Insulin-like growth factor binding protein 6 |
| 26910 | >10 | AA303081 | Hs.78293 | ESTs |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|-----------------|--|--|
| 16938 | >10 | AA059473 | Hs.60763 | ESTs | |
| 41788 | >10 | T03735 | Hs.29885 | ESTs | |
| 7754 | >10 | AA234634 | Hs.16722 | Human NF-IL6-beta protein mRNA complete cds | |
| 6122 | >10 | X72012 | Hs.75962 | Enoglin (Osie-Rendu-Weber syndrome 1) | |
| 2946 | >10 | M52856 | Hs.159 | TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR | |
| 23013 | >10 | T16851 | Hs.6725 | ESTs | |
| 19537 | >10 | H50270 | Hs.32593 | ESTs | |
| 4594 | >10 | U50360 | EST - U50360 | EST | |
| 37410 | >10 | AA453652 | Hs.99344 | ESTs | |
| 27969 | >10 | AA464594 | Hs.63382 | ESTs | |
| 35497 | >10 | AA400006 | Hs.144344 | EST | |
| 37013 | >10 | AA439890 | Hs.130268 | ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens] | |
| 39247 | >10 | AA621563 | Hs.112968 | ESTs | |
| 13471 | >10 | AA452598 | Hs.109590 | ESTs | |
| 42110 | >10 | T68878 | Hs.76868 | Carboxylesterase 2 (liver) | |
| 10965 | >10 | AA128597 | Hs.18953 | Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA complete cds | |
| 4918 | >10 | U67733 | Hs.3831 | Human GMP-stimulated 3'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds | |
| 40737 | >10 | N51950 | Hs.81454 | H.sapiens KHK mRNA for ketohexokinase clone pHKK3a | |
| 30403 | >10 | N45300 | Hs.110547 | Msl1 (mouse) homolog | |
| 11432 | >10 | AA233369 | Hs.361 | ESTs | |
| 18794 | >10 | F09748 | Hs.7374 | ESTs | |
| 40662 | >10 | NA9281 | EST - RC_N45281 | EST | |
| 5773 | >10 | X54162 | Hs.79386 | 64 KD AUTOANTIGEN D1 | |
| 35041 | >10 | AA350566 | Hs.30862 | ESTs | |
| 20668 | >10 | N70068 | Hs.7243 | ESTs | |
| 39729 | >10 | H11489 | Hs.105005 | ESTs | |
| 27397 | >10 | AA426330 | Hs.76264 | ESTs | |
| 39758 | >10 | H13614 | Hs.80485 | Human apM1 mRNA for GS3105 (novel adipose specific collagen-like factor) complete cds | |
| 4319 | >10 | U37293 | Hs.59882 | Human microfini-associated glycoprotein-2 MAGP-2 mRNA complete cds | |
| 2866 | >10 | M59815 | Hs.76982 | Complement component 4A | |
| 30332 | >10 | N39075 | Hs.44924 | EST | |
| 41344 | >10 | RA0199 | Hs.6985 | ESTs | |
| 29271 | >10 | AA521200 | Hs.46776 | ESTs | |
| 5834 | >10 | X57129 | Hs.7644 | HISTONE H1D | |
| 13046 | >10 | H05464 | Hs.100251 | ESTs | |
| 1429 | >10 | J02884 | Hs.9315 | Human 20 kDs myosin light chain (MLC-2) mRNA complete cds | |
| 19431 | >10 | H27510 | Hs.107364 | ESTs | |
| 29992 | >10 | N26395 | Hs.33084 | Solute carrier family 2 (facilitated glucose transporter) member 5 | |
| 2041 | >10 | L36033 | Hs.77423 | Stomach cell-derived factor 1 | |
| 22655 | >10 | R99009 | Hs.36196 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|----------|-------------------|--|--|
| 11624 | AA243854 | Hs.17098 | ESTs | |
| 12512 | AA405199 | Hs.20733 | ESTs | |
| 41443 | R45577 | Hs.10683 | ESTs | |
| 5005 | U77180 | Hs.50002 | Human mRNA for EBI1-ligand chemokine complete cds | |
| 8038 | X86045 | Hs.746 | Basic fibroblast growth factor (bFGF) receptor (shorter form) | |
| 42520 | U72359 | Hs.74659 | ESTs Weakly similar to SYNAPTOTREBIN 2 [H.sapiens] | |
| 827 | D87433 | Hs.84753 | Human mRNA for KIAA0246 gene partial cds | |
| 830 | D78014 | Hs.74586 | Human mRNA for dihydromyristase related protein-3 complete cds | |
| 650 | AA452806 | Hs.92380 | EST | |
| 37350 | AA455178 | Hs.90397 | ESTs | |
| 37488 | AA431797 | Hs.98763 | EST | |
| 38648 | AA606007 | EST - RC_AA009607 | | |
| 38909 | AA487895 | Hs.17311 | ESTs | |
| 38191 | N67484 | Hs.74970 | Human mRNA for KIAA0146 gene partial cds | |
| 5944 | | Hs.107374 | ESTs | |
| 8130 | AA341723 | Hs.111301 | N-CHIMAERIN | |
| 41522 | RG3586 | Hs.70092 | Matrix metalloproteinase 2 (matrilase A 72kD gelatinase 72kD type IV collagenase) | |
| 38960 | AA452603 | EST - RC_R09241 | | |
| 41175 | R02241 | ESTs | | |
| 35847 | AA437388 | Hs.115726 | ESTs | |
| 4175 | U26553 | Hs.17610 | Pigment epithelium-derived factor | |
| 35421 | AA359886 | Hs.97669 | EST | |
| 4358 | U39487 | Hs.250 | Xanthine dehydrogenase | |
| 35463 | AA400272 | Hs.97758 | EST | |
| 7026 | Z80345 | Hs.127610 | Asyl-Coenzyme A dehydrogenase C-2 to C-3 short chain | |
| 34825 | AA282238 | Hs.116463 | Homo sapiens clone 24519 unknown mRNA partial cds | |
| 20179 | N24879 | Hs.9693 | ESTs | |
| 36805 | AA435901 | Hs.58674 | ESTs Weakly similar to p20 protein [R.norvegicus] | |
| 24447 | W83121 | Hs.23841 | Human mRNA for KIAA0335 gene complete cds | |
| 10247 | R74386 | Hs.108924 | ESTs | |
| 3618 | U02388 | Hs.101 | Leukotriene B4 omega hydroxylase (cytochrome P450 subfamily 1F) | |
| 18730 | F08876 | Hs.8008 | ESTs | |
| 22529 | R73075 | Hs.29327 | EST | |
| 37520 | AA455960 | Hs.99405 | ESTs | |
| 41122 | R05483 | Hs.139500 | ESTs | |
| 4417 | U42311 | Hs.7557 | Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds | |
| 9742 | M14777 | Hs.89552 | Glutathione S-transferase A2 | |
| 36194 | AA421142 | Hs.104672 | ESTs | |
| 4445 | U43563 | Hs.3261 | Leplin (murine obesity homolog) | |
| 19749 | H53728 | Hs.38608 | ESTs | |
| 19793 | H56965 | Hs.34564 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|--------------------|--|--|
| 12713 | >10 | AA418398 | Hs.17778 | ESTs | |
| 1464 | >10 | J03474 | Hs.3157 | SERUM AMYLOID A PROTEIN PRECURSOR | |
| 16942 | >10 | AA055163 | Hs.57975 | Homo sapiens mRNA for cardiac calcineurin complete cds | |
| 34229 | >10 | AA234383 | Hs.3576 | ESTs | |
| 35553 | >10 | AA401404 | Hs.112087 | ESTs | |
| 46735 | >10 | AA045305 | Hs.42956 | ESTs | |
| 33007 | >10 | W63497 | Hs.59466 | ESTs | |
| 10146 | >10 | AA052236 | Hs.60162 | ESTs | |
| 22656 | >10 | R55880 | Hs.33455 | ESTs | |
| 22562 | >10 | R77493 | Hs.29953 | EST | |
| 22985 | >10 | T16211 | Hs.6326 | Homo sapiens clones 23798 and 23825 mRNA sequence | |
| 5248 | >10 | U85358 | Hs.30404 | Human diemokine (TECK) mRNA complete cds | |
| 27608 | >10 | AA443800 | Hs.43125 | ESTs | |
| 7510 | >10 | AA139353 | Hs.38022 | ESTs | |
| 34683 | >10 | AA284920 | Hs.13716 | ESTs | |
| 27633 | >10 | AA446659 | Hs.2953 | Tachykinin 2 (substance K neurokinin A neurokinin 2 neuromedin L neurokinin alpha neuropeptide K neuropeptide gamma) | |
| 32485 | >10 | T16335 | Hs.65325 | EST | |
| 38791 | >10 | AA069018 | Hs.112629 | ESTs | |
| 32020 | >10 | N85796 | Hs.55181 | ESTs | |
| 19866 | >10 | H89980 | Hs.12112 | ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus] | |
| 30748 | >10 | N52254 | Hs.47438 | ESTs | |
| 8903 | >10 | AF002246 | Hs.21225 | Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds | |
| 95959 | >10 | N75215 | Hs.43148 | ESTs | |
| 38136 | >10 | AA486185 | Hs.125176 | ESTs | |
| 19845 | >10 | H59887 | Hs.35167 | ESTs | |
| 1127 | >10 | HG3117- | EST - HG3117-HT383 | | |
| 23637 | >10 | T85315 | Hs.15903 | ESTs | |
| 16599 | >10 | AA043349 | Hs.62630 | ESTs | |
| 36702 | >10 | AA434108 | Hs.101303 | ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 (Homo sapiens) | |
| 28930 | >10 | F02702 | Hs.141503 | Small Inducible cytokine A5 (RANTES) | |
| 9226 | >10 | D62584 | Hs.109439 | ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR (bos laurus) | |
| 3357 | >10 | N59447 | Hs.1915 | PROSTATE-SPECIFIC MEMBRANE ANTIGEN | |
| 36783 | >10 | AA435605 | EST | | |
| 4876 | >10 | U65061 | Hs.112055 | EST | |
| 41149 | >10 | R06986 | Hs.2048 | Prolinase srime 2 (trypsin 2) | |
| 22200 | >10 | R54179 | Hs.75487 | ESTs | |
| 15625 | >10 | Y13492 | Hs.26100 | ESTs | |
| 10911 | >10 | AA113387 | Hs.75483 | Homo sapiens mRNA for smoothelin | |
| 3336 | >10 | N97675 | Hs.24305 | ESTs | |
| 31859 | >10 | N91697 | Hs.1844 | Human protein tyrosine kinase t-Ror (Ror1) mRNA complete cds | |
| | >10 | | Hs.50652 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|----------------|--|--|
| 10406 | >10 | AA076629 | Hs.25478 | ESTs | |
| 17737 | >10 | AA142875 | Hs.71719 | ESTs | |
| 38939 | >10 | AA009632 | Hs.112737 | EST | |
| 16206 | >10 | AA010511 | Hs.60418 | EST | |
| 32810 | >10 | W15376 | Hs.122856 | ESTs | |
| 18210 | >10 | AA159306 | Hs.86045 | ESTs | |
| 24054 | >10 | W15590 | Hs.15342 | ESTs | |
| 23047 | >10 | T23457 | Hs.7120 | ESTs | |
| 12944 | >10 | AA248258 | Hs.8769 | ESTs | |
| 34172 | >10 | AA227469 | Hs.139171 | EST | Human mRNA for KIAA0278 gene partial cds |
| 5317 | >10 | D87468 | Hs.40888 | ESTs | |
| 19331 | >10 | H17855 | Hs.23213 | ESTs | |
| 21035 | >10 | N02824 | Hs.14898 | ESTs | |
| 34208 | >10 | AA233380 | Hs.104249 | EST | |
| 5974 | >10 | X64072 | Hs.83958 | Integrin beta 2 (antigen CD18 (p95) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit) | |
| 5032 | >10 | U74382 | Hs.90357 | Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds | |
| 41941 | >10 | T32561 | Hs.5476 | ESTs | |
| 34239 | >10 | AA235709 | Hs.32246 | ESTs | |
| 32852 | >10 | W31906 | Hs.116428 | ESTs | |
| 7652 | >10 | AA203527 | Hs.18747 | Homo sapiens ribonuclease P protein subunit (p20) (RPP20) mRNA complete cds | |
| 6432 | >10 | X89056 | Hs.94413 | Transient receptor potential channel 1 | |
| 37001 | >10 | AA443311 | Hs.98998 | ESTs | |
| 4630 | >10 | U52101 | Hs.9989 | Human YMP mRNA complete cds | |
| 19489 | >10 | H27852 | Hs.28137 | ESTs | |
| 28483 | >10 | C14270 | Hs.68957 | ESTs | |
| 19801 | >10 | H57357 | Hs.18767 | ESTs Weakly similar to unknown protein [H.sapiens] | |
| 24672 | >10 | Z39300 | Hs.124952 | ESTs | |
| 31153 | >10 | N6388 | EST - RC_M6388 | Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) member 1 | |
| 42250 | >10 | H92431 | Hs.110 | ESTs | |
| 20328 | >10 | T17215 | Hs.6952 | ESTs | |
| 28072 | >10 | AA140886 | Hs.86093 | ESTs | |
| 11868 | >10 | AA352556 | Hs.28902 | ESTs Weakly similar to centaurin alpha [R.norvegicus] | |
| 33359 | >10 | AA309061 | Hs.117961 | ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens] | |
| 4285 | >10 | U35139 | Hs.50130 | Human MEDIN related protein mRNA complete cds | |
| 4655 | >10 | U52969 | Hs.80296 | BRAIN SPECIFIC POLYPEPTIDE PER-19 | |
| 28030 | >10 | AA235984 | Hs.87469 | ESTs | |
| 2042 | >10 | L31651 | Hs.1166 | Thrombopoietin (myeloproliferative leukemia virus oncogene ligand megakaryocyte growth and development factor) | |
| 25262 | >10 | AA043201 | Hs.30250 | Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds | |
| 34821 | >10 | AA291983 | Hs.144599 | ESTs | |
| 42405 | >10 | W44682 | Hs.109896 | ESTs | |

FIGURE 7 (CONT.)

| | | | | |
|-------|-----|-----------|--------------|---|
| 41348 | >10 | R40395 | Hs.112125 | lecithin-cholesterol acyltransferase |
| 14454 | >10 | A609645 | Hs.25632 | ESTs Weakly similar to PNG gene [H.sapiens] |
| 4453 | >10 | U43916 | Hs.70368 | Human epithelial membrane protein (CL-20) mRNA complete cds |
| 42758 | >10 | Z41411 | Hs.107040 | ESTs |
| 2098 | >10 | L39009 | EST - L39009 | ESTs |
| 35637 | >10 | AA402933 | Hs.20283 | ESTs |
| 16549 | >10 | AA029697 | Hs.94854 | EST - HG3733-HI4003 |
| 1220 | >10 | HG3733- | Hs.124094 | ESTs |
| 39934 | >10 | H52185 | Hs.109631 | Human tyrosyl-tRNA synthetase mRNA complete cds |
| 7735 | >10 | AA232121 | Hs.108900 | ESTs |
| 40392 | >10 | H99587 | Hs.99145 | EST |
| 37170 | >10 | AA447779 | Hs.86989 | ESTs |
| 19351 | >10 | AA223902 | Hs.133466 | ESTs |
| 19366 | >10 | HT2004 | Hs.108694 | Glycophorin A |
| 38429 | >10 | AA465665 | Hs.105152 | ESTs |
| 36021 | >10 | AA461059 | Hs.67234 | Human lizidol homolog (FZD3) mRNA complete cds |
| 5184 | >10 | U62169 | Hs.70202 | ESTs Weakly similar to FZD3.4 [C.elegans] |
| 27653 | >10 | AA455051 | Hs.96396 | EST |
| 37476 | >10 | D67468 | Hs.40888 | ESTs |
| 27185 | >10 | AA410695 | Hs.62348 | Human mRNA for KIAA0276 gene partial cds |
| 859 | >10 | N80689 | Hs.21639 | Human APEG-1 mRNA complete cds |
| 41010 | >10 | AA499076 | Hs.105101 | ESTs |
| 38241 | >10 | R89477 | Hs.34299 | ESTs |
| 22701 | >10 | AA291271 | Hs.10086 | ESTs Weakly similar to uroporphyrinogen III synthase UROHIS [H.sapiens] |
| 12152 | >10 | AA609531 | Hs.112050 | ESTs |
| 38913 | >10 | AA1192871 | Hs.83760 | Tropoin 1 (skeletal fast) |
| 34034 | >10 | AA459857 | Hs.99503 | EST |
| 4173 | >10 | U29725 | Hs.1632 | CD27L RECEPTOR PRECURSOR |
| 16178 | >10 | AA009639 | Hs.124044 | ESTs |
| 20527 | >10 | N54161 | Hs.102243 | ESTs |
| 41918 | >10 | T25873 | Hs.1501 | Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated fibroglycan) |
| 1525 | >10 | J04621 | Hs.30972 | EST |
| 19160 | >10 | H10208 | Hs.59152 | ESTs Weakly similar to Nats1 [M.musculus] |
| 16860 | >10 | AA0355833 | Hs.104944 | EST |
| 36927 | >10 | AA437259 | Hs.103972 | Salivary proline-rich protein |
| 1595 | >10 | K03207 | Hs.26216 | ESTs |
| 15574 | >10 | V38778 | Hs.24332 | ESTs Weakly similar to deoxyribose-phosphate aldolase [C.elegans] |
| 8995 | >10 | CO0125 | Hs.130088 | Home sapiens FIP2 alternatively translated mRNA complete cds |
| 33995 | >10 | AA182945 | | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|-------------------|--|--|
| 7949 | >10 | AA23820 | Hs.34056 | ESTs | |
| 16607 | >10 | AA034916 | Hs.85079 | ESTs | |
| 11670 | >10 | AA232191 | Hs.25199 | Homo sapiens PAC clone DJ130H16 from 22q12.1-qter | |
| 7354 | >10 | AA092348 | Hs.7858 | ESTs | |
| 4277 | >10 | U34879 | Hs.85279 | ESTRAD10L 17 BETA-DEHYDROGENASE 1 | |
| 22314 | >10 | T40895 | Hs.11937 | Human protein tyrosine phosphatase PTPCAAX1 (HPTPCAAX1) mRNA complete cds | |
| 22209 | >10 | RS4694 | Hs.25209 | ESTs | |
| 38151 | >10 | AA419011 | Hs.98744 | ESTs | |
| 23372 | >10 | T59537 | EST - RC_T59537 | | |
| 42136 | >10 | T72491 | Hs.73849 | Adiponectin C-III | |
| 289 | >10 | D15400 | Hs.73850 | Hydroxy-Coenzyme A dehydrogenase/Glutathyl-Coenzyme A thioester/enoyl Coenzyme A hydratase (trifunctional protein) alpha subunit | |
| 15974 | >10 | Z35531 | Hs.2659 | H-sapiens mRNA for fibronogen-like protein (p140 protein) | |
| 41379 | >10 | R42233 | Hs.106487 | H-mo sapiens mRNA for KIAA0873 protein partial cds | |
| 34764 | >10 | AA237370 | Hs.890 | Lymphodisin-beta | |
| 24027 | >10 | W01875 | Hs.5734 | Homo sapiens mRNA for KIAA0879 protein partial cds | |
| 38197 | >10 | AA421158 | Hs.97514 | ESTs | |
| 37211 | >10 | AA448334 | EST - RC_AA448334 | | |
| 27684 | >10 | AA448525 | Hs.57929 | ESTs | |
| 31790 | >10 | N80279 | Hs.50891 | ESTs | |
| 24515 | >10 | Z38289 | Hs.12701 | ESTs | |
| 18652 | >10 | F03111 | Hs.22505 | ESTs | |
| 16835 | >10 | AA037433 | Hs.46987 | ESTs | |
| 37815 | >10 | AA469952 | Hs.97899 | ESTs | |
| 6384 | >10 | X83857 | Hs.495 | Prostaglandin E receptor 3 (subtype EP3) (alternative products) | |
| 9034 | >10 | C01833 | Hs.29759 | ESTs Weakly similar to HIII ALU SUBFAMILY SX WARNING ENTRY HIII [H sapiens] | |
| 16469 | >10 | AA025728 | Hs.61307 | ESTs | |
| 27034 | >10 | AA400102 | Hs.49051 | ESTs | |
| 42746 | >10 | Z40646 | Hs.124953 | ESTs | |
| 33568 | >10 | AA399269 | Hs.15250 | Homo sapiens DBI-related protein mRNA complete cds | |
| 34805 | >10 | AA331522 | Hs.97250 | EST | |
| 19953 | >10 | H89355 | Hs.6596 | ESTs | |
| 31128 | >10 | N63444 | Hs.47566 | ESTs | |
| 22618 | >10 | R81949 | Hs.124954 | ESTs | |
| 12248 | >10 | AA348198 | Hs.14829 | Homo sapiens mRNA for GABA-B1a (GAB1a) receptor | |
| 8777 | >10 | AA468865 | Hs.7974 | ESTs | |
| 13486 | >10 | AA453034 | Hs.21041 | ESTs Highly similar to FIBROPELIN C PRECURSOR [Strongly/centrosous purpurus] | |
| 25512 | >10 | AA085721 | Hs.95511 | ESTs | |
| 29073 | >10 | F12567 | EST - RC_F12567 | | |
| 5541 | >10 | X07203 | Hs.89151 | CD20 RECEPTOR | |
| 41689 | >10 | R02942 | Hs.107755 | ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli] | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|--------------|--|--|
| 32343 | >10 | R00965 | Hs.125052 | ESTs | |
| 36335 | >10 | AA480916 | Hs.112157 | ESTs | |
| 41729 | >10 | R32458 | Hs.89554 | Hemoglobin gamma-G | |
| 28491 | >10 | AA431246 | Hs.98802 | EST | |
| 28491 | >10 | C14784 | Hs.12392 | ESTs | |
| 41702 | >10 | R86970 | Hs.123363 | ESTs | |
| 32246 | >10 | R52163 | Hs.144526 | ESTs | |
| 17314 | >10 | AA086487 | Hs.107365 | ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens] | |
| 30325 | >10 | N38967 | Hs.44904 | EST | |
| 19823 | >10 | H58692 | Hs.9520 | ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus] | |
| 42153 | >10 | T77729 | Hs.89890 | Private carboxylase | |
| 19321 | >10 | H71511 | Hs.24963 | ESTs | |
| 27110 | >10 | AA404454 | Hs.84112 | CTP synthetase | |
| 28931 | >10 | D58722 | Hs.92924 | ESTs | |
| 6333 | >10 | X02494 | Hs.2653 | Fibulin 2 | |
| 37679 | >10 | AA160981 | Hs.90662 | ESTs | |
| 40829 | >10 | N61344 | Hs.76362 | Human clone 23839 mRNA sequence | |
| 19132 | >10 | H09343 | Hs.27761 | ESTs | |
| 19353 | >10 | H18706 | Hs.31694 | ESTs | |
| 10935 | >10 | AA121534 | Hs.6923 | ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus] | |
| 11621 | >10 | AA243574 | Hs.14691 | ESTs | |
| 36336 | >10 | AA521370 | Hs.104423 | ESTs | |
| 10095 | >10 | R22139 | Hs.30343 | ESTs | |
| 30014 | >10 | N26740 | Hs.42771 | ESTs | |
| 4484 | >10 | U44259 | Hs.19511 | Human D53 (D53) mRNA partial cds | |
| 3850 | >10 | U03977 | Hs.76224 | Human extracellular protein (S1-5) mRNA complete cds | |
| 36377 | >10 | AA426056 | Hs.99450 | ESTs | |
| 20437 | >10 | N50550 | Hs.24587 | Homo sapiens mRNA for E61 complete cds | |
| 1576 | >10 | R02100 | Hs.117050 | ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR | |
| 42078 | >10 | T64891 | Hs.144323 | ESTs | |
| 27257 | >10 | AA418001 | Hs.46146 | ESTs Weakly similar to mitogen-activated kinase kinase 5 [H. sapiens] | |
| 30552 | >10 | N48848 | Hs.46974 | EST | |
| 3631 | >10 | U03050 | Hs.230 | Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds | |
| 19026 | >10 | H04798 | Hs.30484 | ESTs | |
| 4752 | >10 | U59632 | Hs.3547 | Glycoprotein Ib (platelet) beta polypeptide | |
| 3766 | >10 | U08579 | Hs.74994 | CYCLIN-DEPENDENT KINASE INHIBITOR 1 | |
| 1437 | >10 | J02923 | Hs.76506 | Lymphocyte cytosolic protein 1 (L-plasin) | |
| 33905 | >10 | AFFX- | AFFX-TpnlX.5 | | |
| 4310 | >10 | U37055 | Hs.76034 | Macrophage stimulating 1 (hepatocyte growth factor-like) | |
| 26923 | >10 | AA342302 | Hs.55036 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|-----|----------|-----------|--|
| 5520 | >10 | X08256 | Hs.119218 | Integrin alpha 5 (fibronectin receptor alpha polypeptide) |
| 37571 | >10 | AA457409 | Hs.59458 | EST |
| 38800 | >10 | AA609052 | Hs.112636 | EST |
| 27052 | >10 | AA463700 | Hs.47042 | Homo sapiens CD39L3 (CD39L3) mRNA complete cds |
| 27621 | >10 | AA446242 | Hs.56589 | ESTs |
| 38764 | >10 | AA608988 | Hs.2051 | Testis specific protein Y-linked |
| 201 | >10 | D16532 | Hs.73729 | Very low density lipoprotein receptor |
| 18014 | >10 | AA173168 | Hs.57672 | ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans] |
| 16720 | >10 | AA044732 | Hs.7208 | ESTs |
| 25336 | >10 | AA053405 | Hs.101044 | ESTs |
| 39653 | >10 | AA658909 | Hs.1009 | ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 5659KD isoform 1 |
| 13419 | >10 | H56010 | Hs.108144 | ESTs Weakly similar to [H.sapiens] |
| 42373 | >10 | AA463504 | Hs.652 | ESTs |
| 1403 | >10 | AA450336 | Hs.22369 | ESTs |
| 42373 | >10 | J00123 | Hs.93587 | PROENKEPHALIN A PRECURSOR |
| 13777 | >10 | W35362 | Hs.103012 | ESTs |
| 13419 | >10 | R28267 | Hs.24255 | ESTs |
| 21520 | >10 | M63509 | Hs.73974 | Oxidation S-transferase M2 (muscle) |
| 9798 | >10 | AA404271 | Hs.22631 | Human glutamate receptor (GLUR5) mRNA complete cds |
| 35650 | >10 | W69586 | Hs.103156 | ESTs |
| 42501 | >10 | Z41239 | Hs.106960 | ESTs |
| 33812 | >10 | W65731 | Hs.122531 | ESTs |
| 42473 | >10 | AA033700 | Hs.75336 | Apolipoprotein D |
| 25195 | >10 | C21481 | Hs.94530 | ESTs Moderately similar to [H.sapiens] SQ WARNING ENTRY [H.sapiens] |
| 28807 | >10 | U07620 | Hs.95681 | Human MAP kinase mRNA complete cds |
| 3712 | >10 | X77307 | Hs.2507 | 5-HYDROXYTRYPTAMINE 2B RECEPTOR |
| 6214 | >10 | T80833 | Hs.14794 | ESTs |
| 23575 | >10 | N9765 | Hs.50947 | ESTs |
| 31775 | >10 | U82979 | Hs.67846 | Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds |
| 5206 | >10 | R94521 | Hs.124693 | ESTs |
| 22769 | >10 | H12574 | Hs.9395 | ESTs |
| 29288 | >10 | H61046 | Hs.70405 | EST Moderately similar to [H.sapiens] WARNING ENTRY [H.sapiens] |
| 9377 | >10 | AA147537 | Hs.4911 | ESTs |
| 11081 | >10 | T33511 | Hs.4844 | ESTs |
| 41980 | >10 | H77754 | Hs.38702 | Homo sapiens roundabout 1 (robo1) mRNA complete cds |
| 29416 | >10 | AA489218 | Hs.105229 | ESTs |
| 38248 | >10 | AA449424 | Hs.98428 | ESTs |
| 37256 | >10 | R43980 | Hs.26320 | ESTs |
| 21611 | >10 | T34622 | Hs.8708 | ESTs Weakly similar to HYPOTHETICAL 35.9 KD PROTEIN IN PRP16-SRP40 INTERGENIC REGION [S.carassius] |
| 23184 | >10 | AA011305 | Hs.10029 | Cathepsin C |
| 16225 | >10 | | | |

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FIGURE 7 (CONT.)

| | | | | | |
|--------|-----|----------|-------------------|--|--|
| 27766 | >10 | A4453556 | Hs.89417 | ESTs | |
| 16071 | >10 | A4001426 | Hs.43853 | ESTs | |
| 17343 | >10 | A4100152 | Hs.5921 | ESTs | |
| 10643 | >10 | A4040154 | Hs.32478 | ESTs | |
| 260335 | >10 | H68239 | Hs.39422 | ESTs | |
| 340866 | >10 | A4344868 | Hs.1285 | Complement component 8 gamma polypeptide | |
| 263003 | >10 | A4255463 | Hs.88042 | EST | |
| 1030 | >10 | H62416- | EST | EST - HG2416-HT2542 | |
| 28370 | >10 | A4605559 | Hs.38550 | ESTs | ESTs Moderately similar to alpha subunit [H sapiens] |
| 25303 | >10 | H68861 | Hs.39427 | ESTs | |
| 21076 | >10 | N99976 | Hs.80015 | ESTs | |
| 27100 | >10 | A4404231 | EST - RC_AA04231 | ESTs | |
| 11329 | >10 | A4216589 | Hs.28462 | ESTs | |
| 4402 | >10 | U41518 | Hs.74602 | AQUAPORIN-CHIP | |
| 11050 | >10 | AA142819 | Hs.5558 | ESTs | |
| 22844 | >10 | R98947 | EST - RC_R98947 | ESTs | |
| 31581 | >10 | N71371 | Hs.39938 | ESTs | |
| 7253 | >10 | AA074407 | Hs.139119 | ESTs | |
| 29423 | >10 | N48008 | Hs.104938 | ESTs | |
| 39254 | >10 | AA621750 | EST - RC_AA621750 | ESTs | |
| 36415 | >10 | AA426598 | Hs.24897 | Homo sapiens chromosome 21q22.1 anonymous mRNA sequence | |
| 16575 | >10 | AA031948 | Hs.57548 | ESTs | |
| 37505 | >10 | AA455659 | Hs.103233 | ESTs | |
| 28254 | >10 | AA521080 | Hs.46765 | ESTs | |
| 23896 | >10 | T95325 | Hs.16545 | ESTs | |
| 11781 | >10 | AA256485 | Hs.33413 | ESTs | |
| 25603 | >10 | AA114250 | Hs.48924 | Homo sapiens mRNA for KIAA0512 protein complete cds | |
| 9003 | >10 | C03808 | Hs.107842 | ESTs | |
| 5632 | >10 | X15357 | EST - X15357 | ESTs | |
| 7680 | >10 | AA206945 | Hs.8059 | ESTs | |
| 22783 | >10 | R95689 | Hs.35437 | ESTs | |
| 20852 | >10 | N95540 | Hs.17713 | ESTs | |
| 16795 | >10 | AA047896 | Hs.49169 | ESTs | |
| 37558 | >10 | AA456575 | Hs.75736 | ApoE/apoprotein D | |
| 35957 | >10 | AA412537 | Hs.98149 | EST | |
| 47129 | >10 | T71561 | Hs.84824 | ESTs | |
| 34585 | >10 | AA381002 | Hs.40735 | ESTs | |
| 33690 | >10 | Z38607 | Hs.62246 | ESTs | |
| 8904 | >10 | AF022256 | Hs.86180 | Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds | |
| 2689 | >10 | MG3273 | Hs.1756 | Arylsulfatase B | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|---|--|--|
| 40909 | >10 | N69064 | Hs.45608 | ESTs | |
| 23377 | >10 | RG3090 | Hs.26391 | ESTs | |
| 21208 | >10 | R07651 | Hs.20023 | EST | |
| 27304 | >10 | AA421783 | Hs.58908 | Homo sapiens mRNA for zinc finger protein FPM315 complete cds | |
| 3307 | >10 | M95809 | Hs.89578 | BASIC TRANSCRIPTION FACTOR 62 KO SUBUNIT | |
| 25370 | >10 | AA057556 | Hs.28478 | ESTs | |
| 41423 | >10 | R41717 | Hs.22917 | ESTs | |
| 2570 | >10 | M27160 | Hs.2053 | Tyrosinase (oculocutaneous albinism 1A) | |
| 14557 | >10 | AA620965 | Hs.108300 | ESTs highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus] | |
| | >10 | Z79291 | EST - Z79291 | | |
| 7023 | >10 | N52696 | Hs.48607 | EST | |
| 31051 | >10 | AA621246 | Hs.112556 | EST | |
| 39200 | >10 | Z39652 | Hs.27457 | ESTs | |
| 24712 | >10 | T52497 | Hs.9444 | ESTs Moderately similar to III; ALU CLASS A WARNING ENTRY III; [H sapiens] | |
| 23296 | >10 | AA424806 | Hs.134646 | ESTs | |
| 12826 | >10 | L49169 | Hs.75678 | Human GUS3 mRNA complete cds | |
| 2199 | >10 | AA119767 | Hs.43498 | ESTs | |
| 27226 | >10 | AA028976 | Hs.8175 | ESTs | |
| 7135 | >10 | AA074955 | EST - RC_AA074955 | | |
| 17102 | >10 | AA609646 | Hs.94970 | Human mRNA for KIAA0306 gene partial cds | |
| 38942 | >10 | H64973 | Hs.30336 | ESTs | |
| 22988 | >10 | AA250843 | Hs.54434 | Interferon regulatory factor 5 | |
| 34338 | >10 | N63566 | Hs.47681 | ESTs | |
| 30818 | >10 | AA045461 | Hs.65093 | ESTs | |
| 16748 | >10 | T07569 | Hs.113025 | ESTs | |
| 42317 | >10 | L77663 | EST - L77563 | | |
| 2228 | >10 | N55971 | Hs.47927 | ESTs | |
| 30662 | >10 | AA119536 | Hs.97561 | ESTs | |
| 33954 | >10 | AA426303 | Hs.98467 | ESTs | |
| 36403 | >10 | AA441812 | Hs.88959 | ESTs | |
| 36949 | >10 | R70212 | Hs.73630 | immunoglobulin-associated alpha | |
| 41628 | >10 | AA621076 | Hs.111956 | ESTs | |
| 39175 | >10 | AA460147 | EST - RC_AA460147 | | |
| 31657 | >10 | AA424242 | Hs.98397 | ESTs Weakly similar to precursor of major fibrous sheath protein [M.musculus] | |
| 36279 | >10 | Z18954 | Hs.2360 | \$100 calcium-binding protein A5 (formerly S100D) | |
| 6834 | >10 | N33212 | Hs.107197 | ESTs | |
| 40562 | >10 | AA463272 | Hs.22636 | ESTs | |
| 13770 | >10 | U79249 | Human clone 23839 mRNA sequence | | |
| 5101 | >10 | Hs.78362 | Human transducin-like enhancer protein (TLE3) mRNA complete cds | | |
| 3355 | >10 | M69438 | Hs.31305 | ESTs | |
| 8478 | >10 | AA442119 | Hs.29790 | ESTs | |

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| | | | | |
|-------|----------|---|-------------------|-----|
| 34321 | Hs.15772 | Glucocorticoid receptor | ESTs | >10 |
| 42946 | Hs.05966 | Carbamoyl-phosphate synthetase 1 mitochondrial | ESTs | >10 |
| 23913 | Hs.17749 | TRANSFORMING PROTEIN RHOB | ESTs | >10 |
| 27946 | Hs.15122 | ESTs | EST - RC_AA255523 | >10 |
| 34407 | Hs.42636 | ESTs | ESTs | >10 |
| 16542 | AA255523 | ESTs | ESTs | >10 |
| 6248 | AA029428 | Glycerol kinase 2 (testis specific) | Hs.61535 | >10 |
| 6227 | Hs.78712 | MAmre-6-phosphate receptor (cation dependent) | Hs.98008 | >10 |
| 6248 | Hs.75709 | MAmre-6-phosphate receptor (cation dependent) | Hs.75709 | >10 |
| 3307 | Hs.78774 | ESTs | EST - S78774 | >10 |
| 40907 | Hs.68830 | ESTs | Hs.25717 | >10 |
| 33340 | W73698 | ESTs | Hs.59550 | >10 |
| 19079 | Hs.6371 | ESTs | Hs.20345 | >10 |
| 3392 | U19713 | Allograft inflammatory factor 1 | Hs.76364 | >10 |
| 36059 | AA417063 | ESTs | Hs.98189 | >10 |
| 37634 | AA459662 | ESTs | Hs.99489 | >10 |
| 41581 | R62313 | ESTs Weakly similar to R1P60 [R.noregicus] | Hs.126270 | >10 |
| 38734 | AA608792 | ESTs | Hs.112591 | >10 |
| 37636 | AA470135 | ESTs | Hs.112238 | >10 |
| 21303 | R11157 | ESTs | Hs.12610 | >10 |
| 20125 | N22006 | ESTs | Hs.6202 | >10 |
| 35516 | AA400795 | ESTs | Hs.97450 | >10 |
| 26771 | AA284087 | EST | Hs.80267 | >10 |
| 33358 | W67335 | EST | Hs.59332 | >10 |
| 42625 | Hs.17329 | ESTs | Hs.441 | >10 |
| 26152 | W89426 | ESTs | Hs.10128 | >10 |
| 31968 | N63845 | ESTs | Hs.87762 | >10 |
| 17763 | Hs.16213 | ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus] | Hs.35932 | >10 |
| 21959 | AA4949 | ESTs | Hs.17073 | >10 |
| 10000 | N7974 | ESTs | Hs.22396 | >10 |
| 30658 | N51105 | ESTs | Hs.7915 | >10 |
| 17629 | AA131919 | ESTs | Hs.111223 | >10 |
| 30260 | AA423970 | ESTs | Hs.96909 | >10 |
| 285 | D16227 | Hippocalcin-like 1 | Hs.96378 | >10 |
| 26123 | AA243598 | ESTs | Hs.3818 | >10 |
| 34535 | AA279391 | EST | Hs.20887 | >10 |
| 23100 | H07426 | EST | Hs.104425 | >10 |
| 24122 | W46947 | ESTs | Hs.92350 | >10 |
| 19854 | H65942 | ESTs | Hs.4188 | >10 |
| 98594 | Hs.36030 | ESTs | Hs.36030 | >10 |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|---|---|--|
| 22087 | >10 | T16258 | Hs.25420 | ESTs | |
| 5985 | >10 | Hs.34514 | H.sapiens CHML mRNA | | |
| 42461 | >10 | W60008 | Hs.89717 | Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds | |
| 5422 | >10 | X00588 | Hs.77432 | Epidermal growth factor receptor | |
| 16603 | >10 | AA034366 | Hs.144627 | ESTs | |
| 33380 | >10 | V81807 | Hs.58663 | EST | |
| 6931 | >10 | Z46788 | Hs.3232 | H.sapiens mRNA for cyclin II | |
| 19324 | >10 | H17618 | Hs.28180 | ESTs | |
| 32166 | >10 | R41836 | Hs.9657 | ESTs | |
| 39687 | >10 | H69415 | Hs.102160 | EST | |
| 17958 | >10 | AA168917 | Hs.72639 | ESTs | |
| 38669 | >10 | AA69437 | Hs.29385 | ESTs Highly similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cerevisiae] | |
| 1006 | >10 | T78633 | Hs.106518 | ESTs | |
| 23552 | >10 | AA468997 | Hs.157530 | ESTs | |
| 38228 | >10 | HGZ705- | EST - HGZ705-HT2801 | | |
| 1086 | >10 | T91283 | Human APEG-1 mRNA complete cds | | |
| 23915 | >10 | U57099 | Hs.21639 | EST - RC_191283 | |
| 4499 | >10 | N69706 | Hs.142712 | ESTs | |
| 31306 | >10 | AA399633 | Hs.24872 | ESTs | |
| 12389 | >10 | AA279662 | Hs.142462 | ESTs Moderately similar to snRNP protein B [H.sapiens] | |
| 34539 | >10 | N39584 | Hs.17404 | ESTs | |
| 20368 | >10 | AA236868 | Hs.87564 | ESTs | |
| 26070 | >10 | AA488659 | Hs.105686 | ESTs | |
| 38210 | >10 | AA235674 | Hs.88888 | PUTATIVE DNA BINDING PROTEIN A20 | |
| 28025 | >10 | U71207 | Hs.29279 | Homo sapiens clone 24534 eyes absent homolog (Eab1) mRNA, partial cds | |
| 4935 | >10 | U69162 | Hs.84171 | THROMBOPOIETIN RECEPTOR PRECURSOR | |
| 3501 | >10 | S78467 | EST - S78467 | | |
| 14281 | >10 | AA505136 | Hs.12420 | ESTs | |
| 31859 | >10 | N90698 | Hs.54643 | EST | |
| 41104 | >10 | R01398 | Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds | | |
| 5293 | >10 | L89605 | EST - S81957 | | |
| 3543 | >10 | S81957 | ESTs | | |
| 27615 | >10 | AA443958 | Hs.90960 | Homo sapiens mRNA for KIAA0625 protein partial cds | |
| 7152 | >10 | AA036753 | Hs.78494 | ESTs | |
| 16197 | >10 | AA010328 | Hs.39379 | Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds | |
| 20176 | >10 | N24772 | Hs.30213 | Homo sapiens putative transmembrane protein (CLN5) mRNA complete cds | |
| 33586 | >10 | V939015 | Hs.73166 | Teacher Cofins syndrome susceptibility protein | |
| 27765 | >10 | AA418392 | Hs.46784 | ESTs | |
| 12463 | >10 | AA402000 | Hs.20415 | ESTs Weakly similar to GS3786 [H.sapiens] | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|-----------|-------------------|--|--|
| 35302 | >10 | AA424582 | Hs.124985 | ESTs | |
| 23192 | >10 | TU6048 | Hs.3204 | ESTs | |
| 17423 | >10 | AA114071 | Hs.26270 | ESTs | |
| 23464 | >10 | T07026 | Hs.13019 | ESTs | |
| 42762 | >10 | Z41697 | Hs.106286 | ESTs | Chromogranin A (parathyroid secretory protein 1) |
| 32628 | >10 | T56470 | Hs.119190 | ESTs | |
| 12905 | >10 | AA424331 | Hs.20640 | ESTs | |
| 23379 | >10 | AA039893 | Hs.111841 | Human adenyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds | |
| 39318 | >10 | C20617 | Hs.108945 | Homo sapiens mRNA for KIAA0315 protein pallid cdb | |
| 26659 | >10 | H87938 | Hs.75772 | Glucocorticoid receptor | |
| 17907 | >10 | AA1160530 | Hs.72447 | ESTs | |
| 34919 | >10 | AA411011 | Hs.3038 | ESTs | |
| 36838 | >10 | AA436163 | Hs.59551 | Homo sapiens Plg12 (pIG12) mRNA complete cds | |
| 29611 | >10 | H84043 | Hs.41949 | ESTs | |
| 19550 | >10 | H46167 | Hs.31542 | ESTs | |
| 33221 | >10 | W770305 | Hs.54859 | ESTs | |
| 18840 | >10 | F10265 | Hs.13287 | ESTs | |
| 2590 | >10 | M27533 | EST - M27533 | | |
| 7274 | >10 | AA032171 | Hs.6261 | ESTs | |
| 19524 | >10 | H25566 | Hs.83466 | Homo sapiens clone 23579 mRNA sequence | |
| 40571 | >10 | N33558 | Hs.103102 | ESTs Weakly similar to WWP2 [H.sapiens] | |
| 31178 | >10 | N54191 | Hs.46584 | ESTs | |
| 26984 | >10 | N23009 | Hs.43256 | ESTs | |
| 22201 | >10 | R54416 | Hs.140932 | ESTs | |
| 26716 | >10 | AA282593 | Hs.88617 | ESTs | |
| 32463 | >10 | T16497 | Hs.65339 | EST | |
| 37179 | >10 | AA445804 | Hs.99150 | ESTs | |
| 17390 | >10 | AA165173 | Hs.72754 | ESTs | |
| 21934 | >10 | R44449 | Hs.48778 | ESTs | |
| 38792 | >10 | AA435848 | EST - RC_AA435848 | | |
| 34056 | >10 | AA164951 | Hs.110575 | ESTs | |
| 39102 | >10 | AA620674 | Hs.128692 | EST | |
| 26983 | >10 | AA253217 | Hs.41271 | ESTs | |
| 23999 | >10 | H9529 | Hs.18398 | ESTs | |
| 32456 | >10 | T15629 | Hs.63624 | ESTs | |
| 15440 | >10 | W27301 | Hs.111652 | ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermomonas curvula] | |
| 19004 | >10 | H32399 | Hs.30390 | EST | |
| 27939 | >10 | AA453009 | Hs.58831 | ESTs | |
| 18949 | >10 | F10336 | Hs.106399 | ESTs Moderately similar to POG [Musculus] | |
| 13112 | >10 | AA435986 | Hs.18397 | ESTs | |

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FIGURE 7 (CONT.)

| | | | |
|-------|----------|---|--|
| 1850 | L17325 | Hs.278 | Human pre-T/NK cell associated protein (1D12A2) mRNA complete cds |
| 9101 | C17538 | Hs.25536 | ESTs |
| >10 | M5210 | Hs.81428 | Laminin gamma 1 (formerly LAMR2) |
| 2807 | S57153 | Hs.91797 | Retinoblastoma-binding protein 1 [alternative products] |
| >10 | T26444 | Hs.101248 | ESTs |
| 23142 | U56019 | Hs.30941 | Myoethenic syndrome antigen B [human fetal brain mRNA 3477 nt] |
| 5367 | R44234 | Hs.75169 | ESTs |
| 32205 | A3282972 | Hs.87258 | ESTs |
| 26515 | V241127 | Hs.16003 | ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic [M.musculus] |
| 13332 | A3232251 | Hs.123630 | ESTs |
| 34193 | X65753 | Hs.22393 | CELL DIVISION PROTEIN KINASE 8 |
| 5392 | Z40689 | Hs.65973 | ESTs |
| 30764 | V07464 | Hs.59429 | ESTs |
| 34174 | A3344654 | Hs.96837 | ESTs |
| 34664 | A621414 | Hs.110503 | Homo sapiens transmembrane protein mRNA complete cds |
| 14584 | RG3664 | Hs.33416 | EST |
| 22640 | U38372 | Hs.41548 | EST - U38372 |
| 4359 | AA458966 | Hs.117313 | Human MHC Class I region profile rich protein mRNA complete cds |
| 37357 | U60385 | Hs.47606 | Human Meis1-related protein 2 (MRG2) mRNA partial cds |
| >10 | N53043 | Hs.48382 | ESTs |
| 30795 | N59432 | Hs.104059 | EST |
| 30966 | AA181635 | Hs.23017 | ESTs |
| 33981 | M11591 | Hs.112603 | EST |
| 2285 | V64413 | Hs.7571 | Human clones 23920 and 23921 mRNA sequence |
| 24315 | AA608852 | Hs.95002 | Human U1-snRNP binding protein homolog mRNA complete cds |
| >10 | U79271 | Hs.95043 | ESTs |
| 5119 | U44756 | Hs.105042 | ESTs |
| 15037 | AA446000 | Hs.27646 | ESTs |
| 37045 | AA445392 | Hs.27278 | ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos laurus Sus scrofa] |
| 37627 | R44477 | Hs.47390 | EST - RC_R92512_s |
| 21935 | F03689 | Hs.9410 | ESTs |
| 18669 | RG2512 | Hs.47390 | EST |
| 22737 | N51987 | Hs.59890 | EST |
| 30727 | AA001679 | Hs.79351 | Human two P-domain K+ channel TWIK-1 mRNA complete cds |
| 23253 | U90065 | Hs.93675 | ESTs |
| 5254 | AA148523 | EST - RC_AA101056 | |
| 17769 | AA101056 | EST - AF001359.J | |
| 25549 | 84 | Human msgr1-related gene 1 (mrg1) mRNA complete cds | |
| >10 | AF001359 | Hs.82071 | |
| 4656 | U55093 | | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|----------|-------------------|---|--|
| 7697 | >10 | AA214730 | Hs.107256 | ESTs | |
| 36296 | >10 | AA424535 | Hs.86416 | ESTs | |
| 17460 | >10 | AA125701 | Hs.57409 | ESTs | |
| 36976 | >10 | AA442779 | Hs.98983 | ESTs | |
| 10425 | >10 | AA010619 | Hs.16446 | ESTs | |
| 41196 | >10 | R11854 | Hs.20525 | ESTs | |
| 42265 | >10 | T94409 | EST - RC_T94409 | | |
| 33185 | >10 | V69435 | Hs.50009 | EST | |
| 13974 | >10 | AA479299 | Hs.21107 | ESTs | |
| 19668 | >10 | H61560 | EST - RC_H61560 | | |
| 1376 | >10 | HG831- | EST - HG831-HT831 | | |
| 621 | >10 | D6381.3 | Hs.26996 | Human mRNA for rod photoreceptor protein complete cds | |
| 5346 | >10 | U92459 | Hs.95204 | Human metabotropic glutamate receptor 8 mRNA complete cds | |
| 6029 | >10 | X66533 | Hs.77590 | GUANYLATE CYCLASE SOLUBLE RETA-1 CHAIN | |
| 22196 | >10 | R53972 | Hs.26925 | ESTs | |
| 24609 | >10 | Z38900 | Hs.26915 | ESTs | |
| 37196 | >10 | AA448226 | EST - RC_AA448226 | | |
| 26151 | >10 | AA250636 | Hs.108509 | ESTs | |
| 5938 | >10 | X62535 | Hs.74044 | Diacylglycerol kinase alpha (80KD) | |
| 16373 | >10 | AA019603 | Hs.60992 | ESTs | |
| 26356 | >10 | AA609080 | Hs.41595 | ESTs | |
| 20070 | >10 | H96854 | Hs.20423 | ESTs | |
| 17171 | >10 | AA138541 | Hs.71647 | EST | |
| 20069 | >10 | H98769 | Hs.13121 | ESTs | |
| 40855 | >10 | N74604 | Hs.124694 | ESTs | |
| 10194 | >10 | R63545 | Hs.11553 | ESTs Weakly similar to relative type III alcohol dehydrogenase [D melanogaster] | |
| 40200 | >10 | H87229 | Hs.92983 | Guadotropin-releasing hormone (releasing-releasing hormone) | |
| 34983 | >10 | AA347417 | Hs.96909 | EST | |
| 23543 | >10 | T79203 | Hs.14480 | ESTs | |
| 12770 | >10 | AA421778 | Hs.8661 | ESTs | |
| 25985 | >10 | AA017518 | Hs.115241 | Homo sapiens G protein beta 5 subunit mRNA complete cds | |
| 37746 | >10 | AA463927 | Hs.99598 | ESTs | |
| 2370 | >10 | M18505 | Hs.79978 | STERYL-SULFATASE PRECURSOR | |
| 31244 | >10 | M68062 | Hs.49112 | EST | |
| 31716 | >10 | N75507 | Hs.30020 | ESTs Weakly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP17 [Rattus norvegicus] | |
| 26006 | >10 | AA586959 | Hs.59163 | ESTs | |
| 2220 | >10 | L78667 | Hs.63070 | Homo sapiens Gα14 mRNA complete cds | |
| 12404 | >10 | AA403252 | Hs.23786 | ESTs | |
| 41050 | >10 | M62882 | Hs.105494 | ESTs Weakly similar to putative progesterone binding protein [H sapiens] | |
| 2407 | >10 | M18737 | Hs.90703 | GRANZYME A PRECURSOR | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|-----|-----------|-------------------|--|--|
| 23462 | >10 | T66948 | Hs.12992 | ESTs | |
| 18614 | >10 | F02418 | Hs.107614 | ESTs | |
| 40553 | >10 | N32060 | Hs.104010 | Homo sapiens CAG-as1 7 mRNA complete cds | |
| 27826 | >10 | AA4455849 | Hs.61232 | ESTs | |
| 207 | >10 | D12763 | Hs.66 | Suppression of tumorigenicity 2 | |
| 41094 | >10 | N93508 | Hs.102923 | EST | |
| 10845 | >10 | AA094405 | Hs.106313 | ESTs Weakly similar to P24 protein [M.musculus] | |
| 21813 | 10 | R42039 | Hs.23084 | ESTs | |
| 19483 | 10 | AA2203151 | Hs.81796 | ESTs | |
| 17507 | 10 | AA1196419 | Hs.74876 | ESTs | |
| 20957 | 10 | T97487 | Hs.18070 | ESTs | |
| 13317 | 10 | AA448212 | Hs.38095 | ESTs | |
| 28550 | 10 | H98133 | Hs.41352 | ESTs | |
| 38058 | 10 | AF520411 | Hs.141503 | Small inducible cytokine A5 (RANTES) | |
| 29520 | 10 | AA250413 | Hs.85843 | Spenn focus forming virus (SFFV) proviral integration oncogene sp1 | |
| 37975 | 10 | AA460377 | Hs.98816 | ESTs | |
| 31437 | 10 | N68621 | Hs.49573 | ESTs | |
| 32857 | 10 | T68667 | Hs.76889 | ESTs | |
| 34952 | 10 | AA342828 | Hs.73734 | PLATELET GLYCOPROTEIN V PRECURSOR | |
| 28475 | 10 | AA262264 | Hs.87640 | ESTs | |
| 41827 | 10 | T15445 | Hs.95491 | H-sapiens mRNA for F2553.3 kinase like protein from Celigns | |
| 20073 | 10 | H98985 | Hs.111911 | ESTs | |
| 42336 | 10 | T99713 | Hs.139933 | ESTs | |
| 29412 | 10 | AA255224 | Hs.86646 | ESTs | |
| 21352 | 10 | R15660 | Hs.21745 | ESTs | |
| 22563 | 10 | R79239 | Hs.25855 | EST | |
| 34020 | 10 | AA191543 | Hs.144302 | EST | |
| 25913 | 10 | AA161106 | EST - RC_AA161106 | | |
| 82 | 10 | AF000959 | Hs.110903 | Homo sapiens transmembrane protein mRNA complete cds | |
| 37531 | 10 | AA465140 | Hs.99235 | ESTs | |
| 13314 | 10 | AA448169 | Hs.5728 | ESTs | |
| 31430 | 10 | N88610 | EST - RC_N88610 | | |
| 30570 | 10 | N49587 | Hs.45633 | EST | |
| 7302 | 10 | AA089868 | Hs.103568 | EST | |
| 27732 | 10 | AA452167 | Hs.55778 | ESTs | |
| 22533 | 10 | R73468 | Hs.140996 | ESTs | |
| 31079 | 10 | N62969 | Hs.46862 | EST | |
| 35470 | 10 | AA4100393 | Hs.97803 | EST Weakly similar to precursor polypeptide [H.sapiens] | |
| 37102 | 10 | AA448869 | Hs.110316 | ESTs | |
| 203 | 10 | D12820 | Hs.106242 | CYTOCHROME P450 1VF3 | |

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| | | | |
|----|----------|---------------------------------------|--|
| 10 | A023277 | Hs.74847 | ESTs |
| 10 | W57852 | Hs.21288 | ESTs |
| 10 | AA157772 | Hs.72185 | ESTs |
| 10 | U90543 | Human lutropin (LH) mRNA complete cds | |
| 10 | AA417988 | Hs.62781 | ESTs |
| 10 | L76970 | Hs.105910 | Homo sapiens skat7 mRNA complete cds |
| 10 | N55051 | Hs.47315 | EST |
| 10 | AB022867 | Hs.21385 | Human mRNA for KIAA0369 gene complete cds |
| 10 | N87262 | Hs.359 | Zinc finger protein 135 (clone PHZ-17) |
| 10 | AA258130 | Hs.15190 | ESTs |
| 10 | W72653 | Hs.59197 | ESTs |
| 10 | AA079094 | EST - RC_AA079094 | |
| 10 | W88568 | Hs.59359 | Homo sapiens glyoxigen-2 gamma (glyoxigen-2) mRNA complete cds |
| 10 | AA430539 | Hs.87760 | EST - RC_AA089396 |
| 10 | AA068386 | Hs.80548 | ESTs |
| 10 | AA012885 | Hs.60050 | ESTs |
| 10 | N71571 | Hs.1571 | EST |
| 10 | N26401 | Hs.43902 | EST |
| 10 | N39375 | Hs.55015 | EST |
| 10 | AA419279 | Hs.82813 | Colony-stimulating factor 1 (M-CSF) |
| 10 | AA400888 | Hs.7159 | ESTs |
| 10 | AA401630 | Hs.62592 | ESTs |
| 10 | AA504512 | Hs.76852 | ESTs Weakly similar to ZK792.1 [C.elegans] |
| 10 | U32324 | Hs.64310 | Human interleukin-11 receptor alpha chain mRNA complete cds |
| 10 | AA465560 | Hs.87908 | ESTs |
| 10 | AA461119 | Hs.99539 | ESTs |
| 10 | AA040722 | Hs.54421 | Bradykinin receptor B2 |
| 10 | AA401253 | Hs.37677 | ESTs |
| 10 | AA495958 | Hs.59886 | ESTs |
| 9 | F10640 | Hs.12354 | ESTs |
| 9 | N62724 | Hs.48814 | EST |
| 9 | W79524 | Hs.53595 | ESTs |
| 9 | T59005 | Hs.10476 | ESTs |
| 9 | AA397841 | Hs.106879 | ESTs |
| 9 | R41389 | Hs.26159 | EST |
| 9 | N53955 | Hs.48903 | ESTs |
| 9 | ST7370 | Hs.89890 | Pyruvate carboxylase |
| 9 | AA164928 | EST - RC_AA164928 | |
| 9 | N25557 | Hs.93692 | ESTs |
| 9 | H17463 | Hs.101735 | ESTs |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-------------------|---|
| 21481 | 9 | R25141 | Hs.24032 | ESTs Highly similar to transmembrane receptor (H.musculus) |
| 10887 | 9 | AA101632 | Hs.22971 | ESTs |
| 31431 | 9 | N68666 | Hs.76798 | ESTs |
| 30756 | 9 | N52398 | Hs.33252 | ESTs |
| 25829 | 9 | AA111438 | Hs.17435 | Oryzotopsamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydro |
| 25540 | 9 | Z36435 | Hs.19235 | ESTs |
| 37500 | 9 | AA455474 | Hs.100530 | ESTs |
| 19007 | 9 | H03358 | EST - RC_H03358 | |
| 42650 | 9 | W92272 | Hs.25801 | Homo sapiens zinc-finger helixcase (ZF-H) mRNA complete cds |
| 16705 | 9 | AA043875 | Hs.62833 | EST |
| 40275 | 9 | H94647 | Hs.102329 | ESTs |
| 24372 | 9 | W87423 | Hs.33598 | ESTs |
| 9011 | 9 | Co1394 | Hs.106823 | Homo sapiens c10ne 24418 mRNA sequence |
| 40780 | 9 | N59568 | Hs.108107 | ESTs |
| 17177 | 9 | AA079331 | EST - RC_AA079331 | |
| 20878 | 9 | N70305 | Hs.34492 | ESTs |
| 38140 | 9 | AA486273 | Hs.100472 | ESTs |
| 3490 | 9 | S77783 | Hs.73543 | Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds |
| 39112 | 9 | AA620724 | Hs.112890 | ESTs |
| 27347 | 9 | AA424940 | Hs.43590 | ESTs |
| 14747 | 9 | D80364 | Hs.34882 | ESTs |
| 23559 | 9 | T82307 | EST - RC_T82307 | |
| 23379 | 9 | T98262 | EST - RC_T98262 | |
| 27759 | 9 | AA453472 | Hs.95111 | ESTs |
| 36991 | 9 | AA432381 | Hs.97357 | ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE (H.sapiens) |
| 29782 | 9 | AA284161 | Hs.65310 | ESTs |
| 28816 | 9 | AA285145 | Hs.50446 | ESTs |
| 22334 | 9 | R61290 | Hs.25870 | ESTs |
| 28492 | 9 | N22995 | Hs.42829 | ESTs |
| 22845 | 9 | T10194 | Hs.9877 | Homo sapiens mRNA for KIAA0688 protein complete cds |
| 30618 | 9 | N50656 | Hs.93996 | ESTs Highly similar to mosaic protein LR11 (H.sapiens) |
| 29715 | 9 | H98700 | Hs.60887 | ESTs |
| 37490 | 9 | AA457023 | EST - RC_AA457023 | |
| 23284 | 9 | T500492 | Hs.9002 | EST |
| 31001 | 9 | N92200 | Hs.47566 | ESTs |
| 17841 | 9 | AA156109 | Hs.66180 | ESTs |
| 3478 | 9 | S76992 | Hs.104005 | Var 2 oncogene |
| 11605 | 9 | AA043139 | Hs.4663 | ESTs |
| 19002 | 9 | H04822 | Hs.30494 | EST |
| 29533 | 9 | N24162 | Hs.93677 | ESTs |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|-----------|-----------|---|--|
| 26222 | 9 | AA280431 | Hs.88756 | ESTs | |
| 4286 | 9 | U35376 | Hs.37138 | Human repressor transcriptional factor (ZNF89) mRNA complete cds | |
| 42034 | 9 | T56281 | Hs.110460 | Human metallothionein (MT)-I gene | |
| 30447 | 9 | N47439 | Hs.44003 | ESTs | |
| 25238 | 9 | AA039568 | Hs.44003 | EST - RC_AA039568 | |
| 20238 | 9 | N30077 | Hs.14855 | ESTs | |
| 30232 | 9 | N34500 | Hs.44600 | EST | |
| 17017 | 9 | AA069920 | Hs.10039 | EST - RC_AA069920 | |
| 11845 | 9 | AA2259054 | Hs.10039 | ESTs Weakly similar to unknown [S.cerevisiae] | |
| 30229 | 9 | N34457 | Hs.10039 | EST - RC_N34457 | |
| 30737 | 9 | N52137 | Hs.47442 | EST | |
| 30555 | 9 | N46259 | Hs.47442 | EST - RC_N46259 | |
| 981 | 9 | HG2139- | Hs.47442 | EST - HG2139-HT2208_f | |
| 30498 | 9 | N48325 | Hs.93956 | EST | |
| 40434 | 9 | N21461 | Hs.93956 | EST - RC_N21461 | |
| 36788 | 9 | AA435824 | Hs.95594 | Homo sapiens BAC clone RG113D17 from 7p14.p15 | |
| 28991 | 9 | F04652 | Hs.66195 | ESTs | |
| 25942 | 9 | AA234187 | Hs.67267 | ESTs | |
| 30466 | 9 | N47951 | Hs.57485 | ESTs | |
| 19317 | 9 | H17476 | Hs.11615 | ESTs Weakly similar to dual specificity phosphatase [H.sapiens] | |
| 13859 | 8 | AA470066 | Hs.24309 | ESTs Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus] | |
| 23445 | 8 | T65992 | Hs.11722 | EST | |
| 24448 | 8 | W93273 | Hs.9270 | ESTs Weakly similar to isocitryl-diphosphate Delta-isomerase [H.sapiens] | |
| 7583 | 8 | AA167924 | Hs.63559 | ESTs Highly similar to PROTEIN CDC27HS [Homo sapiens] | |
| 22778 | 8 | R64940 | Hs.35372 | ESTs Weakly similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens] | |
| 16439 | 8 | AA048335 | Hs.47954 | Homo sapiens Shab-related delayed-recifier K+ channel alpha subunit (KCNS3) mRNA complete cds | |
| 42395 | 8 | W42733 | Hs.109870 | ESTs | |
| 19691 | 8 | H09887 | Hs.18357 | ESTs | |
| 23690 | 8 | T87648 | Hs.107648 | EST - RC_T87648 | |
| 7111 | 8 | AA018804 | Hs.125175 | ESTs Highly similar to PAS-RELATED PROTEIN RAB-14 [Rattus norvegicus] | |
| 6400 | 8 | X88163 | Hs.5421 | Bradykinin receptor B2 | |
| 42474 | 8 | W63747 | Hs.109918 | H.sapiens TTF mRNA for small G protein | |
| 11425 | 8 | AA233557 | Hs.25511 | Homo sapiens mRNA for Hc-5 partial cds | |
| 27039 | 8 | AA400277 | Hs.46549 | ESTs | |
| 32206 | 8 | R44386 | Hs.91703 | ESTs | |
| 15310 | 8 | W15068 | Hs.7921 | ESTs | |
| 38601 | 8 | AA431337 | Hs.99017 | ESTs | |
| 463 | 8 | D39462 | Hs.50482 | EST - D39462 | |
| 31674 | 8 | N74357 | Hs.48955 | EST | |
| 31182 | 8 | N64339 | Hs.48955 | EST | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------|---|--|
| 13499 | 8 | AA453458 | Hs.7301 | ESTs | |
| 37514 | 8 | AA455514 | Hs.1019 | Parathyroid hormone receptor 1 | |
| 5998 | 8 | X65544 | Hs.75063 | HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2 | |
| 962 | 8 | I-G180- | | EST - HG180-HT180 | |
| 40790 | 8 | N6228 | Hs.3786 | Gliatinate receptor metabotropic 3 | |
| 25700 | 8 | AA131512 | Hs.103820 | EST | |
| 36890 | 8 | AA436706 | Hs.98955 | ESTs | |
| 2809 | 8 | U55267 | Hs.41846 | EV12A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN) | |
| 5920 | 8 | X11885 | Hs.2025 | Transforming growth factor beta 3 | |
| 16643 | 8 | A0032325 | Hs.47200 | ESTs | |
| 32051 | 8 | R01450 | Hs.91061 | ESTs | |
| 33560 | 8 | W90617 | Hs.50120 | ESTs | |
| 5177 | 8 | X75535 | Hs.118884 | 33 KO HOUSEKEEPING PROTEIN | |
| 33000 | 8 | W45531 | Hs.94642 | ESTs | |
| 20086 | 8 | H98701 | Hs.4985 | ESTs | |
| 4590 | 8 | U50534 | Hs.30649 | Human infant brain mRNA clone 13dMAT3 | |
| 37199 | 8 | AA448257 | Hs.97127 | ESTs | |
| 24601 | 8 | Z38644 | Hs.25803 | ESTs | |
| 33589 | 8 | W93074 | Hs.59342 | ESTs | |
| 37369 | 8 | AA453466 | Hs.99330 | ESTs | |
| 5801 | 8 | X55448 | Hs.3116 | H sapiens mRNA for 2.19 gene | |
| 28748 | 8 | D25912 | Hs.74832 | ESTs | |
| 40070 | 8 | H72592 | Hs.77554 | ESTs | |
| 40367 | 8 | H98657 | Hs.75520 | Human mRNA for KIAA0041 gene partial cds | |
| 33609 | 8 | W93585 | Hs.59476 | ESTs | |
| 24502 | 8 | Z38214 | Hs.26946 | ESTs | |
| 11129 | 8 | AA156673 | Hs.15970 | ESTs | |
| 7144 | 8 | AA033659 | Hs.95154 | ESTs | |
| 28584 | 8 | C21221 | Hs.68619 | ESTs Highly similar to METALLOTHIONEIN-1A [Equus caballus] | |
| 22165 | 8 | S28222 | Hs.22003 | ESTs | |
| 31987 | 8 | N94551 | Hs.55090 | ESTs | |
| 32470 | 8 | T15956 | Hs.65289 | EST | |
| 38642 | 8 | AA599152 | Hs.91379 | PTR-ASSOCIATED SPLICING FACTOR | |
| 40438 | 8 | N21684 | Hs.80500 | Human mRNA for KIAA0061 gene partial cds | |
| 34471 | 8 | AA258843 | Hs.111376 | ESTs | |
| 41571 | 8 | R61005 | Hs.115170 | Human sapiens mRNA for GalT4 protein | |
| 31417 | 8 | N68435 | Hs.49516 | ESTs | |
| 23851 | 8 | T97318 | Hs.19037 | ESTs | |
| 7832 | 8 | AA240260 | Hs.26545 | ESTs | |
| 27928 | 8 | AA461093 | Hs.26799 | ESTs Moderately similar to zinc finger protein [R.no vesigius] | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|----|----------|-------------------|--|
| 2017 | 18 | L34219 | Hs. 1933 | Cellular retinaldehyde-binding protein |
| 25530 | 8 | AA098834 | Hs. 83428 | Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) |
| 20556 | 8 | N55189 | Hs. 34081 | ESTs |
| 27036 | 8 | AA400155 | Hs. 142935 | ESTs |
| 22851 | 7 | R65266 | Hs. 33487 | ESTs |
| 33663 | 7 | V55905 | Hs. 59736 | EST |
| 19374 | 7 | H19472 | Hs. 31653 | EST |
| 10275 | 7 | R79356 | Hs. 19280 | ESTs |
| 39471 | 7 | D60265 | Hs. 107894 | ESTs Weakly similar to PROTEIN Q300 [Mus musculus] |
| 25100 | 7 | AA019426 | Hs. 103343 | EST |
| 8828 | 7 | AB002316 | Hs. 65746 | Human mRNA for KIAA0318 gene partial cds |
| 17132 | 7 | AA075674 | EST - RC_AA075674 | |
| 15915 | 7 | Y08858 | Hs. 83577 | Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPN Igandlin homology (PROTEIN DXF34) hypothetical prote |
| 5216 | 7 | AA393089 | Hs. 80723 | ESTs |
| 22512 | 7 | RT1469 | Hs. 29196 | EST |
| 19097 | 7 | H08171 | Hs. 30842 | ESTs |
| 25048 | 7 | AA011041 | Hs. 130843 | ESTs |
| 35353 | 7 | AA398962 | Hs. 97669 | ESTs |
| 31278 | 7 | N63369 | Hs. 49193 | EST |
| 23149 | 7 | T26893 | Hs. 71569 | EST |
| 11880 | 7 | AA262783 | Hs. 22057 | ESTs |
| 17547 | 7 | AA127595 | Hs. 71016 | ESTs |
| 32854 | 7 | W32094 | Hs. 55501 | ESTs |
| 38622 | 7 | AA435978 | Hs. 98952 | EST |
| 35530 | 7 | AA400893 | Hs. 106185 | Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds |
| 3069 | 7 | U14417 | Hs. 41717 | Human Ral guanine nucleotide dissociation stimulator mRNA partial cds |
| 9398 | 7 | H09246 | Hs. 100739 | ESTs |
| 15154 | 7 | U79527 | Hs. 111075 | Human orphan G-protein coupled receptor Dez isoform a mRNA complete cds |
| 21178 | 7 | R06907 | Hs. 19748 | EST |
| 33081 | 7 | W97731 | Hs. 58213 | ESTs |
| 13848 | 7 | AA465664 | Hs. 21323 | ESTs |
| 19650 | 7 | F03220 | Hs. 13258 | ESTs |
| 1979 | 7 | L29339 | Hs. 1954 | Solute carrier family 5 (sodium/glucose cotransporter) member 1 |
| 22603 | 7 | R80545 | Hs. 29978 | ESTs |
| 2418 | 7 | M15907 | Hs. 1817 | Myeloperoxidase |
| 29863 | 7 | D80051 | Hs. 124418 | ESTs |
| 26764 | 7 | AA233926 | Hs. 51501 | ESTs |
| 6544 | 7 | X55677 | EST - X55677 | |
| 33524 | 7 | W81189 | Hs. 59096 | ESTs |
| 18374 | 7 | AA226877 | Hs. 67624 | ESTs |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|------------------|--|--|
| 10108 | 7 | R25069 | Hs.23790 | ESTs | |
| 26178 | 7 | A0251153 | Hs.27910 | Homo sapiens centrosomal Ndc2-associated protein 1 (C-NAP1) mRNA complete cds | |
| 38428 | 7 | A0427505 | Hs.98551 | Human cardiac myosin binding protein-C (MyBP-C) gene complete cds | |
| 29808 | 7 | N21032 | Hs.43931 | EST | |
| 21487 | 7 | Z41186 | Hs.27987 | ESTs | |
| 24909 | 7 | Z35492 | Hs.27250 | ESTs | |
| 26333 | 7 | A0256075 | Hs.82280 | Homo sapiens regulator of G protein signaling 10 mRNA complete cds | |
| 11507 | 7 | A0235466 | Hs.29161 | ESTs | |
| 40387 | 7 | H8460 | Hs.108673 | ESTs | |
| 16112 | 7 | A004377 | Hs.91813 | Human butyrophilin (BTf2) mRNA complete cds | |
| 25413 | 7 | A065096 | EST - RC_A065096 | | |
| 1332 | 7 | A0443844 | Hs.20887 | ESTs | |
| 27236 | 7 | A0417037 | Hs.67805 | ESTs | |
| 21684 | 7 | R38944 | Hs.129672 | ESTs | |
| 9294 | 7 | D82712 | Hs.15301 | ESTs Weakly similar to ANK repeat region of Fowlpox virus BamHI-ori7 protein [C.elegans] | |
| 16896 | 7 | A0057119 | Hs.5091 | Homo sapiens tosinB (DOT1) mRNA partial cds | |
| 20083 | 7 | H98879 | Hs.28029 | ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus] | |
| 30651 | 7 | N51029 | Hs.38872 | ESTs | |
| 22362 | 7 | R62447 | Hs.22123 | ESTs | |
| 21561 | 7 | R33245 | Hs.23076 | ESTs | |
| 21636 | 7 | R37501 | Hs.23900 | ESTs | |
| 21223 | 7 | R08175 | Hs.110130 | Homo sapiens chromosome 19 cosmid F22329 | |
| 32218 | 7 | R45654 | Hs.1339 | Collagen type IV alpha 2 | |
| 13405 | 7 | A0450118 | Hs.25722 | ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens] | |
| 30527 | 7 | N50740 | Hs.47111 | ESTs | |
| 30117 | 7 | N30524 | Hs.44227 | ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY [III [H sapiens] | |
| 31344 | 7 | N67238 | EST - RC_N67238 | | |
| 38119 | 7 | A0465714 | Hs.105669 | ESTs | |
| 33297 | 7 | V73781 | Hs.105715 | ESTs | |
| 6592 | 7 | Z30426 | Hs.82401 | CD69 antigen (early T cell activation antigen) | |
| 9923 | 7 | N44936 | Hs.24550 | ESTs | |
| 27942 | 7 | A0463237 | Hs.13021 | ESTs | |
| 34845 | 7 | A0293420 | Hs.95494 | ESTs Moderately similar to transcription enhancer factor TEF1 [H sapiens] | |
| 28829 | 7 | N21460 | Hs.43905 | ESTs | |
| 15059 | 7 | U53931 | Hs.85290 | Human Interleukin regulatory factor 7 (humirf7) mRNA complete cds | |
| 40441 | 7 | N22063 | Hs.112063 | ESTs | |
| 25095 | 7 | A018937 | Hs.109488 | ESTs | |
| 28411 | 7 | M62840 | Hs.82842 | Acylglyceryl hydrolase (neutrophil) | |
| 1945 | 7 | L25878 | Hs.95449 | Epoxide hydrolase 1 microsomal (xenobiotic) | |
| 42648 | 7 | W92150 | Hs.79310 | Human GAP SH3 binding protein mRNA complete cds | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|-----------|---------------------|------|--|
| 19592 | 7 | H40696 | Hs.33790 | ESTs | Weakly similar to L8004.7 gene product [S.cerevisiae] |
| 23801 | 7 | N20939 | Hs.38759 | ESTs | |
| 15417 | 7 | W26982 | Hs.39330 | ESTs | |
| 39877 | 7 | H39527 | Hs.107696 | ESTs | |
| 23967 | 7 | T97910 | Hs.18184 | EST | |
| 20041 | 7 | H97012 | Hs.11050 | ESTs | |
| 18314 | 7 | A4214510 | Hs.66618 | ESTs | |
| 22452 | 7 | R67370 | Hs.28758 | ESTs | |
| 30496 | 7 | N49294 | Hs.46650 | EST | |
| 26830 | 7 | A4287057 | Hs.49820 | ESTs | |
| 33432 | 7 | W96075 | Hs.39715 | ESTs | |
| 31394 | 7 | N67960 | Hs.49421 | ESTs | |
| 7053 | 6 | Z64721 | Hs.75792 | ESTs | Hemoglobin alpha 1 |
| 33510 | 6 | W08958 | Hs.59134 | EST | |
| 41311 | 6 | U04320 | Hs.123021 | EST | Human Y5 receptor mRNA complete cds |
| 5355 | 6 | R38516 | Hs.124255 | EST | |
| 12545 | 6 | A4106320 | Hs.24702 | ESTs | |
| 23843 | 6 | T02951 | Hs.110422 | ESTs | |
| 21667 | 6 | R38475 | Hs.21408 | ESTs | |
| 17472 | 6 | AA1121704 | Hs.69494 | ESTs | |
| 25646 | 6 | AA126673 | Hs.110341 | ESTs | |
| 32710 | 6 | T07324 | Hs.97021 | EST | |
| 3450 | 6 | ST3840 | Hs.931 | EST | H.sapiens mRNA for fast 2a myosin heavy chain (3' end) |
| 879 | 6 | HG20960 | EST - HG2090-HT2152 | EST | |
| 8151 | 6 | AA348866 | EST - AA348866 | EST | |
| 35380 | 6 | AA359522 | Hs.97671 | ESTs | Weakly similar to T0443.9 [C.elegans] |
| 23788 | 6 | T91047 | Hs.126785 | ESTs | |
| 940 | 6 | HG1496 | EST - HG1496-HT1496 | ESTs | |
| 35696 | 6 | AA412106 | Hs.97349 | ESTs | |
| 16390 | 6 | AA019034 | Hs.94000 | ESTs | |
| 27547 | 6 | AA436613 | Hs.72157 | ESTs | |
| 22528 | 6 | R73036 | Hs.29323 | EST | |
| 25515 | 6 | AA149089 | Hs.96200 | ESTs | Weakly similar to A-kinase anchor protein 95 AKAP95 [R.noveboracensis] |
| 6473 | 6 | AA437346 | Hs.2367 | EST | SHB adaptor protein (a Src homology 2 protein) |
| 35742 | 6 | AA406058 | Hs.97999 | EST | |
| 36538 | 6 | AA430002 | Hs.112044 | ESTs | |
| 17831 | 6 | AA152323 | Hs.71947 | ESTs | |
| 25072 | 6 | AA015799 | Hs.33792 | ESTs | |
| 15632 | 6 | W56102 | Hs.71218 | ESTs | |
| 20442 | 6 | N50027 | Hs.25275 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-------------------|---|
| 28357 | 6 | AA609120 | Hs.58185 | ESTs Weakly similar to The KIAA0447 gene product is related to adenylyl cyclase [H.sapiens] |
| 25022 | 6 | AA007591 | Hs.110227 | ESTs |
| 29334 | 6 | H68150 | Hs.28310 | ESTs |
| 28148 | 6 | AA498875 | Hs.6433 | Homo sapiens clone 24523 mRNA sequence |
| 30744 | 6 | N2195 | Hs.105365 | H.sapiens mRNA for arginine methyltransferase |
| 27577 | 6 | AA442090 | Hs.119295 | ESTs |
| 33472 | 6 | W87469 | Hs.59992 | ESTs |
| 25687 | 6 | AA130867 | Hs.100119 | ESTs |
| 10040 | 6 | AA027317 | Hs.19136 | ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens] |
| 32036 | 6 | W23631 | Hs.55426 | ESTs |
| 17025 | 6 | AA070160 | EST - RC_AA070160 | |
| 22939 | 6 | T10070 | Hs.4317 | Homo sapiens mRNA for KIAA0667 protein partial cds |
| 15803 | 6 | X82332 | Hs.194115 | Human Kox1 gene for zinc finger protein |
| 34510 | 6 | AA322143 | Hs.58094 | H.sapiens mRNA for melanoma growth regulatory protein MIA |
| 11074 | 6 | AA140903 | Hs.23686 | ESTs |
| 12212 | 6 | AA267746 | Hs.22654 | ESTs |
| 16102 | 6 | AA002150 | Hs.59872 | ESTs |
| 31340 | 6 | N87197 | Hs.50125 | EST |
| 18458 | 6 | H24317 | Hs.6526 | ESTs |
| 17533 | 6 | AA127098 | Hs.71057 | EST |
| 22017 | 6 | R46597 | Hs.22703 | ESTs |
| 23887 | 6 | T97519 | Hs.16075 | ESTs Weakly similar to no similarities to reported gene products [H.sapiens] |
| 30298 | 6 | N86130 | Hs.4792 | ESTs Weakly similar to hypothetical protein [H.sapiens] |
| 28773 | 6 | F04014 | Hs.65966 | ESTs |
| 17042 | 6 | AA070397 | EST - RC_AA070397 | |
| 20017 | 6 | N66628 | Hs.37630 | ESTs |
| 16430 | 6 | AA232138 | Hs.118898 | ESTs |
| 28493 | 6 | C14820 | Hs.67186 | EST |
| 30497 | 6 | N48302 | Hs.6852 | EST |
| 32502 | 6 | T16896 | Hs.65373 | ESTs |
| 41324 | 6 | R38804 | Hs.13434 | Homo sapiens clone 24418 mRNA sequence |
| 18418 | 6 | AA220096 | Hs.60480 | ESTs |
| 23822 | 6 | T84046 | Hs.15345 | ESTs |
| 15342 | 6 | W25781 | Hs.8136 | Homo sapiens clone 23698 mRNA sequence |
| 15246 | 6 | W01094 | Hs.64628 | ESTs |
| 2247 | 6 | M10321 | Hs.110802 | VON WILLEBRAND FACTOR PRECURSOR |
| 31906 | 6 | N82943 | Hs.35966 | Homo sapiens CASK mRNA complete cds |
| 9062 | 6 | C06238 | Hs.95665 | Homo sapiens clone 24700 unknown mRNA partial cds |
| 38940 | 6 | AA599142 | Hs.112509 | EST |
| 42822 | 6 | W87801 | Hs.108209 | ESTs |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|---|
| 27508 | 6 | A4460671 | Hs.54837 | ESTs | |
| 7293 | 6 | A4085354 | EST | A4085354 | |
| 27322 | 6 | A4424325 | Hs.40456 | ESTs | |
| 5774 | 6 | X24169 | Hs.82295 | Hs.82295 | Phosphothiohydrazide farnyltransferase phosphothiohydrazide synthetase phosphoribosylaminimidazole synthetase |
| 33466 | 6 | W04164 | Hs.59907 | ESTs | ESTs highly similar to human protein 12-oxylgenase [H.sapiens] |
| 40323 | 6 | H57468 | Hs.103892 | ESTs | Human N-ethylmaleimide-sensitive factor mRNA partial cds |
| 26539 | 6 | A4276548 | Hs.85522 | ESTs | |
| 23579 | 6 | T81059 | Hs.124065 | ESTs | |
| 22435 | 6 | R69706 | Hs.29705 | ESTs | |
| 19596 | 6 | H00542 | Hs.37445 | ESTs | |
| 18607 | 6 | F02345 | Hs.21197 | ESTs | |
| 18991 | 6 | H02554 | Hs.30323 | ESTs | |
| 7810 | 6 | AA248769 | Hs.105709 | ESTs | ESTs highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus] |
| 30810 | 6 | N53419 | Hs.47646 | ESTs | |
| 17996 | 6 | AA169606 | Hs.72815 | ESTs | |
| 26245 | 6 | AA252357 | Hs.87794 | ESTs | |
| 13348 | 6 | AA448257 | Hs.17914 | ESTs | ESTs highly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT [M.musculus] |
| 15034 | 6 | UA3701 | Hs.75403 | 90S RIBOSOMAL PROTEIN L23a | |
| 33962 | 6 | Z41058 | Hs.79248 | ESTs | |
| 33394 | 6 | W84432 | Hs.59670 | ESTs | |
| 31170 | 6 | N64017 | Hs.48911 | ESTs | |
| 40828 | 6 | N64144 | Hs.102749 | EST | |
| 1789 | 6 | L13258 | Hs.936 | Solute carrier family 17 (sodium phosphate) member 2 | |
| 17740 | 5 | AA142922 | Hs.9817 | Homo sapiens Arg/Abi-interacting protein ArgBP2a (ArgBP2a) mRNA complete cds | |
| 9509 | 5 | H06870 | Hs.49683 | ESTs | |
| 15540 | 5 | W30895 | Hs.7535 | ESTs | |
| 27827 | 5 | AA455976 | Hs.42355 | ESTs | |
| 30697 | 5 | N51585 | Hs.47049 | ESTs | |
| 40269 | 5 | H95787 | Hs.108745 | ESTs | |
| 16627 | 5 | AA036779 | Hs.61826 | Homo sapiens clone 23828 mRNA sequence | |
| 20656 | 5 | N62915 | Hs.57572 | ESTs | ESTs weakly similar to myosin heavy chain [C.elegans] |
| 31069 | 5 | N62272 | Hs.48502 | ESTs | |
| 14877 | 5 | T65508 | Hs.14623 | Homo sapiens mRNA for KIA0825 protein partial cds | |
| 31102 | 5 | N63178 | Hs.48728 | ESTs | |
| 22830 | 5 | R08421 | EST | EST - RC_R08421 | |
| 26248 | 5 | AA004607 | Hs.92924 | ESTs | |
| 32145 | 5 | R39510 | Hs.56170 | Homo sapiens clone 24503 mRNA sequence | |
| 27970 | 5 | AA464626 | Hs.10247 | Activated leukocyte cell adhesion molecule | |
| 34069 | 5 | AA262974 | Hs.111354 | ESTs | |
| 25522 | 5 | H05338 | Hs.90250 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|----------------|---|---|
| 32159 | 5 | R40074 | Hs.124270 | ESTs | |
| 35492 | 5 | A4400514 | Hs.97505 | ESTs | |
| 37630 | 5 | A4439649 | Hs.59405 | ESTs | |
| 27103 | 5 | A4404262 | Hs.63401 | ESTs | ESTs Weakly similar to kynurenine/alpha-aminoindipate aminotransferase [R.novaeigius] |
| 17209 | 5 | A4002933 | Hs.002933 | EST - RC_A4002933 | |
| 589 | 5 | D50930 | Hs.5004 | Human mRNA for KIAA040 gene complete cds | |
| 17489 | 5 | AA122394 | Hs.70811 | ESTs | |
| 6293 | 5 | X30078 | Hs.95262 | Human kappa B mRNA complete cds | |
| 5067 | 5 | U77845 | Hs.21254 | Human hTRIP (hTRIP) mRNA complete cds | |
| 23060 | 5 | T23513 | Hs.71147 | ESTs | |
| 28902 | 5 | D00990 | Hs.45247 | ESTs | |
| 33228 | 5 | R75401 | Hs.92262 | ESTs | |
| 33218 | 5 | W70259 | Hs.48523 | ESTs | |
| 28751 | 5 | D45455 | Hs.65524 | ESTs | |
| 21400 | 5 | R19360 | Hs.14651 | ESTs | |
| 15557 | 5 | W36290 | Hs.9115 | ESTs | |
| 12631 | 5 | AA412293 | Hs.21258 | ESTs | |
| 32282 | 5 | R82579 | Hs.62264 | ESTs | |
| 10416 | 5 | AA009809 | Hs.37599 | ESTs | |
| 40308 | 5 | H96306 | Hs.32990 | Human mRNA for BST-1 complete cds | |
| 11599 | 5 | AA242829 | Hs.7508 | ESTs | |
| 33220 | 5 | W70279 | Hs.54611 | ESTs Weakly similar to 3-oxoacyl-CoA-carrier protein reductase [E.coli] | |
| 23100 | 5 | T23667 | Hs.7316 | ESTs | |
| 15333 | 5 | W24154 | Hs.6166 | ESTs | |
| 8331 | 5 | AA412556 | EST - AA412556 | | |
| 9010 | 5 | C01360 | Hs.67384 | Human sapiens clone 23904 mRNA sequence | |
| 4660 | 5 | U53225 | Hs.75283 | Sorting nexin 1 | |
| 25713 | 5 | AA035444 | Hs.10543 | Human sapiens clone 24505 mRNA sequence | |
| 25242 | 5 | AA039833 | Hs.10941 | Mylasthenic syndrome antigen B [human fetal brain mRNA 3477 nt] | |
| 28708 | 5 | D20539 | Hs.90185 | EST | |
| 7435 | 5 | AA096112 | Hs.26236 | ESTs | |
| 26538 | 5 | AA095990 | Hs.101442 | ESTs Highly similar to ZINC FINGER PROTEIN 6 [human sapiens] | |
| 271 | 5 | D14823 | EST - D14823 | | |
| 5400 | 5 | X04571 | Hs.2230 | Epidermal growth factor | |
| 16812 | 5 | F10040 | Hs.13251 | ESTs | |
| 23393 | 5 | T32318 | Hs.11110 | ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens] | |
| 23446 | 5 | T56282 | Hs.12607 | ESTs | |
| 35204 | 5 | AA396155 | Hs.97900 | ESTs | |
| 31369 | 5 | N67596 | Hs.156395 | ESTs | |
| 5244 | 5 | U05992 | Hs.67197 | Human clone IMAGE:35527 unknown protein mRNA [partial cds] | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|---|---|---|
| 20835 | 5 | N89215 | Hs.37456 | ESTs | |
| 16502 | 5 | A027059 | Hs.61425 | EST | |
| 23691 | 5 | T87693 | Hs.16414 | ESTs | |
| 31642 | 5 | N50188 | Hs.54593 | EST | |
| 7845 | 5 | AA249811 | EST - AA249811 | | |
| 29297 | 5 | H85459 | Hs.38323 | ESTs | |
| 7953 | 5 | AA238403 | Human sapiens mRNA for KIAA0554 protein partial cds | | |
| 38412 | 5 | AA426464 | Hs.74750 | ESTs | |
| 10387 | 5 | H18029 | Hs.98466 | ESTs | |
| 18299 | 5 | A015258 | EST - RC_H18029 | | |
| 25312 | 5 | A047070 | Hs.95278 | EST - RC_AA010258 | |
| 27617 | 5 | AA448114 | Hs.55409 | ESTs | ESTs Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens] |
| 42432 | 5 | YH6403 | Hs.107293 | ESTs | |
| 38432 | 5 | AA496983 | Hs.78972 | Laminin alpha 4 | |
| 32215 | 5 | R45175 | Hs.117183 | ESTs | |
| 15214 | 5 | U93553 | Hs.91310 | Human alpha 1-fetoprotein transcription factor (hFTF) mRNA complete cds | |
| 15141 | 5 | U78796 | Hs.90957 | Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds | |
| 20052 | 5 | H97922 | Hs.5376 | Human LAR-interacting protein 1a mRNA complete cds | |
| 7551 | 5 | AA156839 | Hs.107941 | ESTs | |
| 28451 | 5 | AA259058 | Hs.43616 | ESTs | |
| 42355 | 5 | W20404 | Hs.55405 | ESTs | |
| 39480 | 5 | D60419 | Hs.81915 | STATHMIN | |
| 17369 | 5 | AA101833 | Hs.69293 | EST | |
| 14993 | 5 | U22172 | Hs.73046 | Human DNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds | |
| 23400 | 5 | T63336 | Hs.105095 | ESTs | |
| 21153 | 5 | R05315 | Hs.11923 | EST - RC_R05315 | |
| 14282 | 5 | AA505141 | EST - RC_R01081 | | |
| 21104 | 5 | R01081 | EST - RC_R01081 | | |
| 32825 | 5 | W20364 | Hs.55412 | ESTs | |
| 35018 | 5 | AA349591 | EST - RC_AA349591 | | |
| 25104 | 5 | AA019598 | Hs.103351 | ESTs | |
| 19235 | 5 | H12725 | Hs.31181 | ESTs | |
| 34979 | 5 | AA347209 | Hs.7841 | Human mRNA for KIAA0324 gene partial cds | |
| 21501 | 5 | R26855 | Hs.24120 | ESTs | |
| 18331 | 5 | AA219543 | Hs.10081 | Human sapiens mRNA for KIAA0541 protein partial cds | |
| 37529 | 5 | AA456112 | Hs.99410 | ESTs | |
| 19532 | 5 | W28644 | Hs.9246 | ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BUSC-CSPA INTERGENIC REGION [E.citrius coli] | |
| 11858 | 5 | AA292308 | Hs.105395 | ESTs | |
| 29450 | 5 | H09865 | Hs.111026 | Phosphatidylinositol glycan class F | |
| 37294 | 5 | AA450127 | Hs.110571 | ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD10 [Mus musculus] | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|-----------|-------------------|--|
| 35170 | 5 | AA397830 | Hs.06347 | ESTs Weakly similar to rhp-1 [H.sapiens] |
| 23201 | 5 | T40562 | Hs.8279 | ESTs |
| 27012 | 5 | AA33987.3 | Hs.45231 | ESTs |
| 28767 | 5 | D45508 | Hs.83792 | Surfactant pulmonary-associated protein D |
| 17777 | 5 | AA149634 | Hs.83768 | ESTs Weakly similar to hypothetical L1 protein [H.sapiens] |
| 20588 | 5 | N58079 | Hs.36218 | ESTs |
| 20356 | 5 | N39453 | Hs.27371 | ESTs |
| 23375 | 5 | T59670 | Hs.10615 | EST |
| 17030 | 5 | AA070188 | EST - RC_AA070188 | |
| 30782 | 5 | NG3240 | Hs.118064 | EST |
| 25608 | 5 | AA149226 | Hs.95821 | Human osteoblast stimulating factor mRNA complete cds |
| 31345 | 5 | N67288 | Hs.50139 | ESTs |
| 30784 | 5 | N62857 | Hs.47558 | ESTs |
| 13707 | 5 | AA460281 | Hs.14697 | ESTs |
| 29199 | 5 | H25761 | Hs.57082 | EST |
| 30003 | 4 | AA659920 | Hs.112765 | EST |
| 41529 | 4 | RS4458 | Hs.2959 | Glypican 1 |
| 3151 | 4 | MB3652 | Hs.53155 | Progranulin P factor complement |
| 33134 | 4 | W61284 | Hs.57829 | ESTs |
| 29196 | 4 | H24456 | Hs.85053 | Homo sapiens clone 24440 mRNA sequence |
| 12863 | 4 | AA425762 | Hs.27973 | ESTs |
| 31925 | 4 | AA279627 | Hs.125035 | ESTs |
| 35258 | 4 | N92924 | Hs.125032 | ESTs |
| 39638 | 4 | AA3398428 | Hs.97628 | ESTs |
| 30796 | 4 | H27216 | Hs.107635 | ESTs |
| 19464 | 4 | N53046 | Hs.97146 | ESTs Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens] |
| 42486 | 4 | H24453 | Hs.32085 | EST |
| 34274 | 4 | W68410 | Hs.108657 | Calbindin 2 (28kD calretinin) |
| 37648 | 4 | AA238352 | Hs.110821 | ESTs |
| 3169 | 4 | AA459917 | Hs.99506 | EST |
| 10326 | 4 | MB5065 | Hs.693 | Clearage stimulation factor 3' pre-RNA subunit 2 64kD |
| 15063 | 4 | R96417 | Hs.107795 | ESTs |
| 23571 | 4 | U56814 | Hs.89646 | Homo sapiens DNase gamma mRNA complete cds |
| 14377 | 4 | T85628 | Hs.106169 | ESTs |
| 22255 | 4 | AA599563 | Hs.15299 | ESTs Weakly similar to HSM-2 [H.sapiens] |
| 39620 | 4 | AA435068 | Hs.98849 | ESTs |
| 35053 | 4 | AA358015 | Hs.98998 | ESTs Weakly similar to bilthoraxod [D.melanogaster] |
| 12376 | 4 | AA3399271 | Hs.19610 | ESTs |
| 31406 | 4 | N88163 | Hs.43455 | EST |

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[illegible]

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-------------------|--|
| 32968 | 4 | T59284 | Hs.2314 | Mannose-binding lectin soluble (epsonic defect) |
| 33912 | 4 | W38051 | EST - RC_W38051 | |
| 16320 | 4 | AA011549 | Hs.47864 | ESTs |
| 22696 | 4 | H97938 | Hs.42344 | ESTs |
| 8232 | 4 | AA397529 | EST - AA397529 | |
| 23594 | 4 | AA112320 | Hs.16704 | ESTs |
| 30078 | 4 | N56862 | Hs.46761 | EST |
| 40579 | 4 | N43524 | Hs.102516 | ESTs |
| 8026 | 4 | AA301842 | Hs.105189 | ESTs Weakly similar to reverse transcriptase homolog [H.sapiens] |
| 3094 | 4 | M77481 | Hs.72879 | Human antigen (IMAGE-1) gene complete cds |
| 17480 | 4 | AA121974 | EST - RC_AA121974 | |
| 15766 | 4 | W95777 | Hs.50804 | ESTs |
| 34965 | 4 | AA299603 | Hs.111498 | EST |
| 28779 | 4 | N20290 | Hs.42836 | ESTs |
| 6547 | 4 | X95905 | Hs.9568 | Human mRNA for KIAA0385 gene complete cds |
| 24479 | 4 | W95222 | Hs.34192 | ESTs |
| 16135 | 4 | AA004805 | Hs.63968 | Human Toll-like receptor 2 (TLR2) mRNA complete cds |
| 11098 | 4 | AA151243 | Hs.38163 | ESTs |
| 14386 | 4 | AA599742 | Hs.21600 | ESTs |
| 36078 | 4 | AA417275 | Hs.98214 | ESTs |
| 23440 | 4 | T95566 | Hs.12859 | ESTs |
| 20863 | 4 | N69989 | Hs.19167 | ESTs |
| 20347 | 4 | N39117 | Hs.12250 | ESTs |
| 7795 | 4 | AA247455 | Hs.15220 | ESTs |
| 10729 | 4 | AA054087 | Hs.18858 | ESTs |
| 12734 | 4 | AA419200 | Hs.5737 | ESTs |
| 24446 | 4 | W93119 | Hs.19512 | ESTs |
| 30734 | 4 | N52083 | Hs.47418 | EST |
| 20841 | 4 | N62353 | Hs.109685 | ESTs |
| 21183 | 4 | R05769 | Hs.19795 | ESTs |
| 18138 | 4 | AA192757 | Hs.131687 | ESTs |
| 35110 | 4 | AA396952 | Hs.97302 | ESTs |
| 39497 | 4 | D80154 | Hs.65340 | ESTs |
| 29866 | 4 | N22343 | Hs.43145 | ESTs |
| 8707 | 4 | AA476995 | Hs.76982 | Human sapiens mRNA for KIAA0583 protein partial cds |
| 19472 | 4 | AA333369 | Hs.72158 | ESTs |
| 24720 | 4 | Z39754 | Hs.23238 | ESTs |
| 40825 | 4 | N53923 | Hs.102746 | ESTs |
| 15375 | 4 | W26395 | Hs.58676 | ESTs |
| 32959 | 4 | W35211 | Hs.54801 | ESTs |

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| | | | |
|---|-----------|-----------|--|
| 4 | US2426 | Hs.74597 | Homo sapiens GOK (STIM1) mRNA complete cds |
| 4 | AA256616 | Hs.31707 | ESTs |
| 4 | R33841 | Hs.24709 | ESTs Highly similar to NUCLEOLYSIN TW-1 [Homo sapiens] |
| 4 | K03474 | | EST - K03474 |
| 4 | R01069 | Hs.14603 | ESTs |
| 4 | T15359 | Hs.106443 | ESTs |
| 4 | AA359501 | Hs.103849 | ESTs |
| 4 | AA406231 | Hs.100113 | Human mRNA for KIAA0381 gene partial cds |
| 4 | D20261 | Hs.00067 | ESTs |
| 4 | AA425372 | Hs.108904 | Human mRNA for histone H1x complete cds |
| 4 | AA330634 | | EST - RC_AA330634 |
| 4 | Z35278 | Hs.25236 | Hsapiens PEBP2aC1 acute myeloid leukaemia mRNA |
| 4 | N89848 | Hs.54543 | ESTs |
| 4 | AA015620 | Hs.30807 | ESTs |
| 4 | AA069566 | Hs.67317 | ESTs |
| 4 | W06445 | Hs.58844 | ESTs |
| 4 | AA447612 | Hs.60435 | ESTs |
| 4 | AA253383 | Hs.87734 | ESTs |
| 4 | AA3397616 | Hs.107245 | ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus] |
| 4 | AA287097 | Hs.25114 | ESTs |
| 4 | D88155 | Hs.97196 | Human steroidogenic factor 1 mRNA complete cds |
| 4 | N52979 | Hs.51919 | Plasminogen-like protein |
| 4 | AA454115 | Hs.6000 | ESTs |
| 4 | N69730 | Hs.12160 | ESTs |
| 4 | H94266 | Hs.9451 | ESTs |
| 4 | R95778 | Hs.92008 | EST |
| 4 | AA487165 | Hs.105706 | EST |
| 4 | AA442669 | | EST - AA442669 |
| 4 | AA232646 | Hs.68061 | ESTs |
| 4 | AA010070 | Hs.60339 | EST |
| 4 | S94755 | Hs.09359 | ESTs Moderately similar to type II human keratin a3 [H.sapiens] |
| 4 | W82769 | Hs.104133 | GABRA receptor gamma 3 subunit [human fetal brain mRNA Partial 1596 nt] |
| 3 | AA233172 | Hs.87619 | ESTs |
| 3 | W92001 | Hs.120969 | ESTs |
| 3 | AA447759 | Hs.134724 | ESTs |
| 3 | H10047 | Hs.22515 | ESTs |
| 3 | AA421360 | Hs.27567 | ESTs Weakly similar to similar to alpha-13-nanosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans] |
| 3 | AA074897 | | EST - AA074897 |
| 3 | F04252 | Hs.22137 | ESTs |
| 3 | N77904 | Hs.44380 | ESTs |
| 3 | | | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-----------|--|
| 14971 | 3 | U10493 | Hs.438 | Human Mex1 protein (MOX1) mRNA complete cds |
| 11217 | 3 | AA180487 | Hs.62440 | ESTs |
| 16782 | 3 | AA047265 | Hs.82582 | Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds |
| 21477 | 3 | R20094 | Hs.23531 | ESTs |
| 21382 | 3 | R16896 | Hs.89615 | PROTEIN KINASE C THETA TYPE |
| 19508 | 3 | H28966 | Hs.2507 | EST - RC_H28966 |
| 30301 | 3 | N36174 | Hs.23153 | 5-HYDROXYTRYPTAMINE 2B RECEPTOR |
| 21553 | 3 | R33005 | Hs.2023 | ESTs Weakly similar to ETX1 (alternatively spliced) [H. sapiens] |
| 6102 | 3 | X70340 | Hs.2023 | Transforming growth factor alpha |
| 23502 | 3 | T70580 | Hs.13759 | ESTs |
| 8333 | 3 | AA412620 | Hs.4248 | ESTs |
| 30500 | 3 | N48329 | Hs.30490 | ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F0638.3 IN CHROMOSOME III [Caenorhabditis elegans] |
| 21431 | 3 | R22057 | Hs.23336 | ESTs |
| 35620 | 3 | AA412290 | Hs.98124 | ESTs |
| 12065 | 3 | AA263907 | Hs.110480 | Homo sapiens clone 23837 mRNA sequence |
| 19156 | 3 | H10069 | Hs.25924 | Homo sapiens clone 24466 mRNA sequence |
| 24844 | 3 | Z41301 | Hs.23530 | ESTs |
| 33178 | 3 | W68946 | Hs.141719 | EST |
| 2052 | 3 | L36418 | Hs.75309 | Islet-1 polyphosphate phosphatase-like protein 1 (51C protein) |
| 15327 | 3 | N32474 | Hs.23362 | ESTs |
| 18874 | 3 | F10565 | Hs.7345 | ESTs |
| 9030 | 3 | C02049 | Hs.165291 | ESTs |
| 37470 | 3 | AA454935 | Hs.39566 | ESTs |
| 19167 | 3 | H10941 | Hs.23528 | ESTs |
| 34686 | 3 | AA303078 | Hs.84479 | Human GT334 protein (GT334) gene mRNA complete cds |
| 30591 | 3 | N49552 | Hs.136717 | ESTs |
| 26997 | 3 | AA399488 | Hs.93090 | ESTs |
| 18647 | 3 | F03004 | Hs.27109 | ESTs |
| 17867 | 3 | AA157291 | Hs.72153 | ESTs |
| 15280 | 3 | W07019 | Hs.35088 | ESTs |
| 20465 | 3 | N51599 | Hs.14633 | ESTs |
| 11047 | 3 | AA142949 | Hs.22690 | ESTs |
| 19451 | 3 | H23747 | Hs.31697 | ESTs |
| 41821 | 3 | R69233 | Hs.101504 | ESTs |
| 2822 | 3 | M55621 | Hs.117946 | N-acetylglucosaminyltransferase I |
| 28675 | 3 | D20186 | Hs.74876 | ESTs |
| 13528 | 3 | AA478441 | Hs.11590 | ESTs |
| 29473 | 3 | H83094 | Hs.40478 | ESTs |
| 25629 | 3 | AA151621 | Hs.110694 | ESTs |
| 28532 | 3 | C20980 | Hs.68513 | EST |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------------|------|--|
| 32376 | 3 | R01391 | Hs.64301 | ESTs | |
| 12054 | 3 | A0283848 | Hs.11367 | ESTs | Weakly similar to KIAA0009 [H.sapiens] |
| 15547 | 3 | U32012 | Hs.20933 | ESTs | |
| 40294 | 3 | Hs6073 | Hs.108724 | ESTs | Highly similar to HYPOTHETICAL 55.1 KO PROTEIN IN FAB1-PESA INTERGENIC REGION [Saccharomyces cerevisiae] |
| 22981 | 3 | R06906 | Hs.30152 | ESTs | |
| 15525 | 3 | U28763 | Hs.16349 | ESTs | Human sapiens KIAA0431 mRNA partial cds |
| 17988 | 3 | A161496 | Hs.72695 | EST | |
| 35356 | 3 | U12707 | Hs.2157 | EST | Wiskott-Aldrich syndrome (eczema-thrombocytopenia) |
| 4326 | 3 | U42351 | Hs.75871 | ESTs | Human sapiens protein kinase C-binding protein RACK7 mRNA partial cds |
| 29784 | 3 | N20468 | Hs.42849 | ESTs | ESTs Weakly similar to linc-1 protein ORF2 [H.sapiens] |
| 7692 | 3 | A0262100 | EST - A0262100 | ESTs | |
| 15279 | 3 | U05746 | Hs.133302 | ESTs | |
| 42054 | 3 | T63364 | Hs.9225 | ESTs | ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parastichopus parvimeis] |
| 17943 | 3 | A1165117 | Hs.20509 | ESTs | |
| 4596 | 3 | U50743 | Hs.19520 | ESTs | Sodium/potassium ATPase gamma subunit |
| 16421 | 3 | A0022541 | Hs.61146 | ESTs | |
| 4914 | 3 | U67611 | EST - U67611 | ESTs | |
| 38171 | 3 | A0487301 | Hs.105713 | EST | |
| 20168 | 3 | N24106 | Hs.2759 | ESTs | Cardilage linking protein 1 |
| 18791 | 3 | F09892 | Hs.12575 | ESTs | |
| 24281 | 3 | W79773 | Hs.16511 | ESTs | |
| 13996 | 3 | A0480907 | Hs.15769 | ESTs | |
| 20563 | 3 | N57797 | Hs.34421 | ESTs | |
| 37181 | 3 | A0448158 | Hs.99152 | EST | |
| 21450 | 3 | R23146 | Hs.23456 | ESTs | |
| 19634 | 3 | H44866 | Hs.31597 | ESTs | |
| 10163 | 3 | R54534 | Hs.7898 | ESTs | Human sapiens clone 23938 mRNA sequence |
| 7059 | 3 | Z56810 | EST - Z56810 | ESTs | |
| 25792 | 3 | A0136066 | Hs.91797 | ESTs | Retinoblastoma-binding protein 1 [alternative products] |
| 27426 | 3 | A0428900 | Hs.92897 | ESTs | |
| 29023 | 3 | F09302 | EST - RC_F09302 | ESTs | |
| 10989 | 3 | A0132366 | Hs.8023 | ESTs | Human sapiens mRNA for SPOC |
| 6597 | 3 | X97748 | EST - X97748 | ESTs | |
| 8722 | 3 | A0481309 | Hs.30204 | ESTs | |
| 21476 | 3 | R26085 | Hs.23823 | ESTs | |
| 14096 | 3 | A0487558 | Hs.8135 | ESTs | |
| 35392 | 3 | A0399962 | Hs.97566 | ESTs | |
| 28698 | 3 | C21509 | Hs.112774 | ESTs | |
| 13350 | 3 | A0449297 | Hs.6944 | ESTs | ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens] |
| 41202 | 3 | R12806 | Hs.113619 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-------------------|--|--|
| 15612 | 3 | W51955 | Hs.73372 | ESTs | |
| 33930 | 3 | AA168939 | Hs.95870 | ESTs | |
| 34215 | 3 | AA233855 | Hs.104252 | UTROPHIN | |
| 19208 | 3 | H11734 | Hs.110454 | ESTs Weakly similar to coded for by C. elegans cDNA cm10a3 [C.elegans] | |
| 24047 | 3 | W15366 | Hs.26750 | ESTs | |
| 14852 | 3 | T20999 | Hs.100383 | ESTs highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus] | |
| 27815 | 3 | AA455370 | Hs.59729 | ESTs | |
| 22910 | 3 | R11713 | Hs.11482 | ESTs highly similar to F11 antigen [H.sapiens] | |
| 37510 | 3 | AA455896 | Hs.2699 | Glypican 1 | |
| 37925 | 3 | AA471073 | Hs.104536 | ESTs | |
| 13321 | 3 | AA448238 | Hs.16714 | ESTs | |
| 25699 | 3 | AA235375 | Hs.87151 | EST | |
| 9738 | 3 | M13160 | Hs.99900 | MAS1 oncogene | |
| 16248 | 3 | AA011125 | Hs.10871 | ESTs | |
| 27582 | 3 | AA443856 | Hs.61979 | ESTs Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens] | |
| 16546 | 3 | AA023452 | Hs.35162 | ESTs | |
| 16981 | 3 | AA064859 | EST - RC_AA064859 | | |
| 22126 | 3 | R51021 | Hs.23161 | Homo sapiens retinoic acid hydroxylase mRNA complete cds | |
| 23312 | 3 | T54617 | EST - RC_T54617 | | |
| 16763 | 3 | F09741 | Hs.124205 | ESTs | |
| 10306 | 3 | R68920 | Hs.127565 | ESTs | |
| 22516 | 3 | R71892 | Hs.25996 | ESTs highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus] | |
| 8255 | 3 | AA400226 | Hs.25024 | ESTs Weakly similar to estrogen-responsive finger protein cfp [H.sapiens] | |
| 16361 | 3 | AA019218 | Hs.10550 | ESTs Moderately similar to proto-cadherin 3 [R.norvegicus] | |
| 5453 | 3 | X02910 | Hs.2037 | Tumor necrosis factor | |
| 22509 | 3 | R71393 | Hs.29190 | ESTs | |
| 20065 | 3 | H96657 | Hs.27291 | ESTs | |
| 31091 | 3 | N63076 | Hs.138749 | EST | |
| 39050 | 3 | AA510112 | Hs.124549 | ESTs | |
| 2463 | 3 | M22819 | Hs.77385 | MYOSIN LIGHT CHAIN ALKALINE SMOOTH-MUSCLE ISOFORM | |
| 30159 | 3 | N32623 | Hs.44069 | ESTs | |
| 28913 | 3 | F01950 | Hs.22583 | ESTs highly similar to corepressor protein [M.musculus] | |
| 12257 | 3 | AA350030 | Hs.4221 | ESTs | |
| 3359 | 3 | D26350 | Hs.75119 | Human mRNA for type 2 inositol 145-trisphosphate receptor complete cds | |
| 23587 | 3 | T81358 | Hs.14906 | ESTs | |
| 14323 | 3 | AA598575 | Hs.12851 | ESTs | |
| 27231 | 3 | AA416036 | Hs.7491 | Homo sapiens methionine synthase reductase (MTRR) mRNA complete cds | |
| 34914 | 3 | AA338729 | Hs.133096 | ESTs | |
| 21233 | 3 | R08359 | Hs.19308 | ESTs | |
| 23660 | 3 | T86475 | Hs.16193 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|--------------|--|
| 14236 | 3 | AA095891 | Hs.5011 | ESTs Weakly similar to The hsa1237 gene product is related to S pombe rad21 gene product. [H sapiens] |
| 17617 | 3 | AA131394 | Hs.4672 | ESTs Weakly similar to The KIAA0147 gene product is related to adenoviral cyclase. [H sapiens] |
| 24584 | 3 | Z38804 | Hs.2255 | ESTs Highly similar to OPIOD BINDING PROTEINCELL ADHESION MOLECULE PRECURSOR [Bos taurus] |
| 7426 | 3 | AA095885 | Hs.111818 | Homo sapiens heat shock factor binding protein 1 HSBP1 mRNA complete cds |
| 34871 | 3 | AA300451 | Hs.125146 | ESTs |
| 17932 | 3 | AA167251 | Hs.83525 | Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence |
| 24337 | 3 | W06007 | Hs.8876 | ESTs |
| 22589 | 3 | R70580 | Hs.2874 | ESTs |
| 24584 | 3 | Z38522 | Hs.27082 | EST |
| 22348 | 3 | R01750 | Hs.0136 | ESTs |
| 30217 | 3 | N34288 | Hs.44554 | EST |
| 10210 | 3 | R67468 | Hs.131828 | ESTs |
| 22156 | 3 | RS2145 | Hs.25854 | ESTs |
| 18404 | 3 | AA021264 | Hs.60554 | ESTs Moderately similar to sodium-calcium exchanger form 3 [R. norvegicus] |
| 29310 | 3 | H06842 | Hs.88729 | ESTs |
| 15956 | 3 | M26393 | Hs.127610 | Human mRNA for KIAA0008 gene complete cds |
| 9758 | 3 | Z21217 | Hs.77695 | Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain |
| 20917 | 3 | N72295 | Hs.18004 | ESTs |
| 4847 | 3 | U64573 | EST - U64573 | EST - U64573 |
| 22984 | 3 | T10362 | Hs.57958 | ESTs |
| 9806 | 2 | M79462 | Hs.85633 | Probable transcription factor PML (alternative products) |
| 29807 | 2 | N21031 | Hs.42930 | ESTs |
| 39846 | 2 | H02255 | Hs.7268 | Homo sapiens clone 23872 mRNA sequence |
| 22733 | 2 | R02181 | Hs.34558 | EST |
| 23233 | 2 | T41177 | Hs.3410 | Homo sapiens retinoid acid-inducible endogenous retroviral DNA |
| 18548 | 2 | F01360 | Hs.8092 | ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans] |
| 31692 | 2 | N91968 | Hs.39535 | ESTs |
| 18881 | 2 | F10452 | Hs.12254 | ESTs |
| 24553 | 2 | Z38521 | Hs.5428 | ESTs |
| 19289 | 2 | H16568 | Hs.23748 | ESTs |
| 14185 | 2 | AA490911 | Hs.22363 | Homo sapiens dip1 mRNA complete cds |
| 30723 | 2 | N51935 | Hs.47374 | EST |
| 34031 | 2 | AA102614 | Hs.85577 | Human LIM protein MLP mRNA complete cds |
| 18434 | 2 | AA332206 | Hs.50743 | ESTs |
| 14847 | 2 | D20378 | Hs.30731 | EST |
| 41048 | 2 | N92734 | Hs.115985 | ESTs |
| 38157 | 2 | AA486858 | Hs.105702 | EST |
| 33269 | 2 | U73700 | Hs.73803 | IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR |
| 16616 | 2 | AA035446 | Hs.61783 | ESTs |
| 3276 | 2 | M3718 | Hs.76883 | Nitric oxide synthase 3 (endothelial cell) |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------------------|---|------|
| 33022 | 2 | W45976 | Hs.94667 | EST | ESTs |
| 31704 | 2 | N75055 | Hs.14632 | ESTs | ESTs |
| 38713 | 2 | AA006577 | Hs.112575 | ESTs | ESTs |
| 20396 | 2 | N48283 | Hs.12296 | ESTs | ESTs |
| 10010 | 2 | R07373 | Hs.75429 | ESTs | ESTs |
| 22380 | 2 | R93955 | Hs.1432 | Protein kinase C substrate 80K-H | |
| 15935 | 2 | T11377 | Hs.2654 | Flavin-containing monooxygenase 4 | |
| 23957 | 2 | T69525 | Hs.142528 | ESTs | ESTs |
| 30903 | 2 | N57730 | Hs.48058 | EST | ESTs |
| 20938 | 2 | N73988 | Hs.37477 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 5935 | 2 | X92455 | Hs.108338 | CDW52 antigen (CAMPATH-1 antigen) | |
| 18304 | 2 | H19876 | Hs.7973 | ESTs | ESTs |
| 8604 | 2 | AB000463 | Hs.16277 | Homo sapiens mRNA for SH3 binding protein complete cds clone RESA-22A | |
| 41485 | 2 | R49889 | Hs.5260 | ESTs Weakly similar to Q96G8.3 [C.elegans] | |
| 24585 | 2 | Z39406 | Hs.11797 | ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus] | |
| 25403 | 2 | AA063316 | EST - RC_AA063316 | EST - RC_AA063316 | |
| 35773 | 2 | AA092319 | Hs.104747 | ESTs | ESTs |
| 27955 | 2 | AA042957 | Hs.24912 | Homo sapiens bicoid-like (BICD) mRNA complete cds | |
| 16911 | 2 | AA065859 | Hs.60869 | ESTs | ESTs |
| 42315 | 2 | T97353 | EST - RC_T97353 | EST - RC_T97353 | |
| 40832 | 2 | N45231 | EST - RC_N45231 | EST - RC_N45231 | |
| 15722 | 2 | W79346 | Hs.15250 | Homo sapiens DBI-related protein mRNA complete cds | |
| 14942 | 2 | AA417344 | Hs.98220 | ESTs Moderately similar to located at OATL-1 [H.sapiens] | |
| 35065 | 2 | W20796 | Hs.63290 | Phosphodiesterase 6A cAMP-specific rod alpha | |
| 15527 | 2 | R49533 | Hs.133217 | ESTs | ESTs |
| 10302 | 2 | R08773 | Hs.20231 | ESTs | ESTs |
| 27243 | 2 | AA234987 | Hs.64147 | ESTs Weakly similar to F59C6.4 [C.elegans] | |
| 7159 | 2 | N74336 | Hs.97681 | ESTs | ESTs |
| 31572 | 2 | AA264722 | Hs.89121 | ESTs | ESTs |
| 25799 | 2 | AA155504 | Hs.95875 | EST | ESTs |
| 25657 | 2 | AA043115 | Hs.9452 | ESTs Weakly similar to ORF YOL077c [S.cerevisiae] | |
| 16895 | 2 | HG16104 | EST - HG16104-HT-1829 | EST - HG16104-HT-1829 | |
| 964 | 2 | AA401452 | Hs.32050 | ESTs | ESTs |
| 12439 | 2 | H41235 | Hs.109568 | ESTs | ESTs |
| 19599 | 2 | W70158 | Hs.29596 | ESTs | ESTs |
| 24223 | 2 | N83764 | Hs.10175 | ESTs Weakly similar to hypothetical protein [H.sapiens] | |
| 21652 | 2 | AA121338 | EST - RC_AA121338 | EST - RC_AA121338 | |
| 17453 | 2 | F03032 | Hs.65526 | ESTs Weakly similar to reverse transcriptase homolog [H.sapiens] | |
| 28949 | 2 | AA215537 | Hs.104186 | ESTs | ESTs |
| 34140 | 2 | | | | |

FIGURE 7 (CONT.)

| | | | |
|-------|---|----------|--|
| 7465 | 2 | AA120866 | EST - AA120866 |
| 17376 | 2 | AA102425 | EST - RC_AA102425 |
| 5130 | 2 | U79286 | Hs.85953 Homo sapiens clone 24440 mRNA sequence |
| 30041 | 2 | N27628 | Hs.132744 Homo sapiens clone 24525 mRNA sequence |
| 19684 | 2 | I48488 | Hs.143798 ESTs |
| 8196 | 2 | AA359093 | EST - AA359093 |
| 20439 | 2 | H11509 | Hs.22462 ESTs |
| 19202 | 2 | N50785 | Hs.13269 ESTs |
| 20439 | 2 | AA011310 | Hs.3757 ESTs |
| 10431 | 2 | H68244 | Hs.42519 ESTs |
| 29707 | 2 | H37909 | Hs.107680 ESTs |
| 39688 | 2 | C00185 | Hs.10444 ESTs |
| 8968 | 2 | R40442 | Hs.75652 Glutathione S-transferase M5 |
| 41350 | 2 | AA436156 | Hs.110837 ESTs |
| 13121 | 2 | W86550 | Hs.132188 ESTs |
| 15747 | 2 | F03969 | ESTs Weakly similar to KIAA0412 [H.sapiens] |
| 18674 | 2 | HG1019- | EST - HG1019-HT1019 |
| 914 | 2 | T91086 | EST - RC_T91086 |
| 23604 | 2 | AA279089 | Hs.86550 ESTs |
| 26555 | 2 | AA453381 | Hs.104900 ESTs |
| 6567 | 2 | N47686 | Hs.64607 Human RACH1 (RACH1) mRNA complete cds |
| 30457 | 2 | R45441 | Hs.23710 ESTs |
| 21975 | 2 | AA120766 | Hs.70724 ESTs |
| 17452 | 2 | N83495 | Hs.54960 ESTs |
| 31958 | 2 | N69850 | Hs.49759 ESTs |
| 31495 | 2 | T16389 | Hs.81246 Human RNA-binding protein CUG-BP1/Nas50 (NAB50) mRNA complete cds |
| 32490 | 2 | AA621067 | Hs.112944 ESTs |
| 39174 | 2 | R34073 | Zinc finger protein 138 (clone p12-20) |
| 21572 | 2 | Y09466 | V-akt avian sarcoma viral oncogene homolog |
| 15914 | 2 | AA381769 | Hs.81972 Human flipt (FliPST) mRNA complete cds |
| 12014 | 2 | H18412 | Hs.75253 ESTs highly similar to PROTEIN PHOSPHATASE PZZA 55 KO REGULATORY SUBUNIT NEURONAL ISOFORM [Oryctolagus cuniculus] |
| 39777 | 2 | R00176 | Hs.117619 ESTs |
| 9404 | 2 | H09751 | Hs.124027 ESTs |
| 19147 | 2 | AA424179 | Hs.57911 ESTs |
| 36276 | 2 | AA025903 | Hs.20735 ESTs |
| 16475 | 2 | R12208 | Hs.10024 ESTs |
| 21304 | 2 | AA176446 | Hs.85564 ESTs |
| 11199 | 2 | AA187955 | Hs.31040 EST |
| 10093 | 2 | H11274 | EST - W76399 |
| 19190 | 2 | W76399 | |
| 15710 | 2 | | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|--|---|--|
| 18707 | 2 | F04627 | Hs.23540 | ESTs | |
| 6477 | 2 | X91504 | Hs.54904 | Transcription factor COUP 2 (a.k.a. ARP1) | |
| 20323 | 2 | N68869 | Hs.15119 | ESTs | |
| 16336 | 2 | AA018601 | Hs.75649 | EXTRACELLULAR SIGNAL-REGULATED KINASE 3 | |
| 15980 | 2 | H48457 | Hs.35104 | ESTs | |
| 24333 | 2 | Z41087 | Hs.19066 | ESTs | |
| 24056 | 2 | W23709 | Hs.109047 | ESTs | |
| 26180 | 2 | AA251230 | Hs.112272 | ESTs | |
| 37177 | 2 | AA447968 | Hs.7765 | ESTs | |
| 14047 | 2 | AA482597 | Hs.26054 | ESTs | |
| 10770 | 2 | AA056863 | Hs.22552 | ESTs | |
| 41994 | 2 | T47601 | Hs.138605 | ESTs | |
| 19217 | 2 | H12243 | EST - RC | H12243 | |
| 36532 | 2 | AA429869 | Hs.68882 | Acrosin | |
| 23378 | 2 | T60072 | Hs.10688 | ESTs | |
| 1450 | 2 | J03071 | Hs.115352 | Growth hormone 1 | |
| 8007 | 2 | AA293072 | Hs.97283 | ESTs Moderately similar to IIII ALU CLASS B WARNING ENTRY IIII [H. sapiens] | |
| 17266 | 2 | AA084723 | Hs.24812 | ESTs | |
| 24819 | 2 | Z40923 | Hs.69491 | DNA-BINDING PROTEIN A | |
| 6532 | 2 | X95325 | Hs.86641 | ESTs | |
| 26850 | 2 | AA287651 | Hs.108788 | ESTs | |
| 34715 | 2 | AA227523 | Hs.77978 | EST - RC_A4282169 | |
| 34520 | 2 | AA287169 | Hs.15420 | ESTs | |
| 27085 | 2 | AA402455 | Hs.26419 | EST - RC_A4120060 | |
| 20173 | 2 | N24130 | Hs.44076 | Homo sapiens clone 24510 mRNA sequence | |
| 17574 | 2 | AA120060 | Hs.19976 | ESTs | |
| 22300 | 2 | R69200 | Hs.30729 | Peroxidase biogenesis factor 6 | |
| 30970 | 2 | N29699 | Hs.62284 | Human RGP3 mRNA complete cds | |
| 20487 | 2 | N52322 | Hs.23954 | ESTs Weakly similar to D204S.9 [C.elegans] | |
| 724 | 2 | U27655 | Hs.59718 | EST | |
| 4132 | 2 | W95526 | Hs.5723 | ESTs | |
| 33959 | 2 | W95526 | Hs.5723 | ESTs | |
| 13375 | 2 | AA449716 | Hs.94074 | EST | |
| 30991 | 2 | AA480045 | Hs.7534 | ESTs | |
| 13986 | 2 | R99906 | Hs.100530 | Homo sapiens germline mRNA sequence | |
| 22306 | 2 | T33164 | Hs.12840 | ESTs | |
| 23167 | 2 | N70134 | Hs.31476 | ESTs | |
| 20873 | 2 | Hs.8590 | Homo sapiens clone 23718 mRNA sequence | | |
| 7231 | 2 | AA056327 | Hs.8590 | Homo sapiens clone 23718 mRNA sequence | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|--|
| 24582 | 2 | Z38752 | Hs.20330 | ESTs | |
| 11320 | 2 | AA213657 | Hs.22222 | ESTs | |
| 16388 | 2 | AA020781 | Hs.60847 | ESTs | |
| 24608 | 2 | Z38888 | Hs.25046 | ESTs | |
| 7809 | 2 | AA248085 | Hs.12469 | Homo sapiens clone 23330 mRNA sequence | |
| 13163 | 2 | AA437225 | Hs.22410 | ESTs | |
| 20549 | 2 | N54591 | Hs.37591 | ESTs | ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens] |
| 1139 | 2 | HG3227- | | EST - HG3227-HT3404 | |
| 35572 | 2 | AA401489 | | EST - RC_AA401489 | |
| 6964 | 2 | Z49105 | Hs.137591 | H.sapiens HD21 mRNA | |
| 27704 | 2 | AA449704 | Hs.17637 | Homo box A4 | |
| 33196 | 2 | V69725 | Hs.10711 | ESTs | |
| 30963 | 2 | N59373 | Hs.26812 | ESTs | |
| 13896 | 2 | AA476937 | Hs.24441 | ESTs | |
| 18184 | 2 | AA007569 | Hs.75385 | Human mRNA for TPRD complete cds | |
| 18083 | 2 | AA181826 | Hs.70524 | Homo sapiens mRNA for foxq1 protein | |
| 20107 | 2 | Nz1207 | ESTs | ESTs Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus] | |
| 16238 | 2 | T16566 | Hs.125942 | ESTs | |
| 18169 | 2 | AA011670 | Hs.40470 | ESTs | |
| 37567 | 2 | AA195042 | Hs.85978 | ESTs | |
| 2174 | 2 | AA457377 | | EST - RC_AA457377 | |
| 39958 | 2 | L42611 | Hs.111758 | KERATIN TYPE II CYTOSKELETAL 6D | |
| 37919 | 2 | AA059707 | Hs.112751 | ESTs | |
| 28905 | 2 | AA478162 | Hs.104965 | ESTs | |
| 33315 | 2 | D81123 | Hs.57475 | ESTs | |
| 7421 | 2 | W74418 | Hs.55410 | ESTs | |
| 3745 | 2 | AA095900 | | EST - AA095900 | |
| 19545 | 2 | U09117 | Hs.80776 | Human phospholipase c delta 1 mRNA complete cds | |
| 21204 | 2 | H37834 | Hs.32669 | ESTs | |
| 8416 | 2 | R07632 | Hs.17949 | ESTs | |
| 17569 | 2 | AA428531 | | EST - AA428531 | |
| 19572 | 2 | AA128926 | | EST - RC_AA128926 | |
| 22780 | 2 | H39195 | Hs.22223 | ESTs | |
| 19354 | 2 | R93714 | Hs.33833 | ESTs | ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens] |
| 40518 | 2 | H18829 | Hs.121515 | ESTs | |
| 23913 | 2 | N39595 | Hs.108540 | ESTs | |
| 22571 | 2 | N23708 | Hs.43429 | ESTs | |
| 7598 | 2 | R78565 | Hs.138395 | EST | |
| 25395 | 2 | AA174185 | Hs.3354 | Homo sapiens c-erbB-1-mosin binding phosphoprotein-50 mRNA complete cds | |
| | 2 | AA059069 | Hs.106727 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|--|--|
| 14176 | 2 | AA406020 | Hs.11809 | ESTs |
| 37400 | 2 | AA453578 | Hs.120594 | ESTs Weakly similar to T20D3.5 [C.elegans] |
| 29487 | 2 | H85120 | Hs.80881 | N-ACETYLACTOSAMINE SYNTHASE |
| 10197 | 2 | R64199 | Hs.50785 | Homo sapiens vesicle trafficking protein sec22b mRNA complete cds |
| 322 | 2 | D21241 | EST - D21241_xpt1 | |
| 22224 | 2 | R55192 | Hs.25689 | ESTs |
| 19488 | 2 | H27615 | Hs.25604 | ESTs |
| 10568 | 2 | AA029703 | Hs.36574 | ESTs |
| 10872 | 2 | AA069357 | Hs.15780 | ESTs Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus] |
| 29387 | 2 | N36172 | Hs.63760 | ESTs |
| 30709 | 2 | N53143 | Hs.64001 | ESTs |
| 9638 | 2 | L07592 | Hs.106415 | Human peroxisome proliferator activated receptor mRNA complete cds |
| 21069 | 2 | N64061 | Hs.17706 | ESTs |
| 27195 | 2 | AA411473 | Hs.65311 | ESTs |
| 9241 | 2 | D75865 | Hs.56886 | ESTs |
| 9218 | 2 | D61469 | Hs.56886 | ESTs |
| 22238 | 2 | R35763 | Hs.107287 | ESTs |
| 7512 | 2 | AA115508 | Hs.2780 | Jun D proto-oncogene |
| 17438 | 2 | AFFX- | AFFX-HSAC07X00351_M | |
| 24532 | 2 | F01525 | Hs.3786 | Glutamate receptor metabotropic 3 |
| 28911 | 2 | AA125969 | ESTs.34769 | ESTs Weakly similar to F35G12.9 [C.elegans] |
| 10944 | 2 | T86199 | Hs.142702 | ESTs |
| 43224 | 2 | AA287655 | Hs.8245 | ESTs |
| 34756 | 2 | AA421050 | Hs.24545 | ESTs |
| 12743 | 2 | R10075 | Hs.14890 | ESTs |
| 21275 | 2 | AA459389 | Hs.20350 | Homo sapiens mRNA for tyrosyl sulfotransferase-2 |
| 13976 | 2 | AA430474 | Hs.16466 | ESTs |
| 13009 | 2 | AA094921 | Hs.79788 | ESTs |
| 7403 | 2 | AA159901 | Hs.25819 | ESTs |
| 11151 | 2 | AA404707 | Hs.54865 | ESTs |
| 35669 | 2 | AA135941 | Hs.71626 | ESTs |
| 17701 | 2 | F04686 | Hs.21782 | ESTs |
| 18713 | 2 | N52312 | Hs.30303 | ESTs Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens] |
| 24144 | 2 | N52175 | Hs.22222 | ESTs |
| 30741 | 2 | T23433 | Hs.7105 | ESTs |
| 23042 | 2 | AA233483 | Hs.87159 | ESTs |
| 18479 | 2 | AA410355 | Hs.103081 | ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens] |
| 8314 | 2 | AA291796 | ESTs Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens] | |
| 7990 | 2 | Hs.2822 | EST - RC_AA005355 | |
| 10388 | 2 | AA005355 | | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|--|--|
| 9407 | 2 | H20086 | EST - H20086 | |
| 42791 | 2 | AFXC- | AFXC-HUMGAPDH33197_M | |
| 26302 | 2 | AA255470 | ESTs | |
| 30722 | 1 | N51924 | ESTs | |
| 24965 | 1 | AFXC- | AFXC-Lyx5 | |
| 38850 | 1 | AA60262 | EST - RC_AA60262 | |
| 13746 | 1 | AA461300 | ESTs | |
| 6893 | 1 | Z30543 | Hs.30543 Hsapiens mRNA for chloride channel (putative) 213bp | |
| 31403 | 1 | N89147 | Hs.120123 Hsapiens mRNA for chloride channel (putative) 213bp | |
| 17820 | 1 | AA152012 | ESTs | |
| 10593 | 1 | AA033874 | Hs.12035 ESTs | |
| 20913 | 1 | N72116 | Hs.57435 Natural resistance-associated macrophage protein 2 | |
| 35007 | 1 | AA02267 | ESTs Weakly similar to zinc finger protein [H.sapiens] | |
| 9408 | 1 | N44756 | ESTs Weakly similar to transformation-related protein [H.sapiens] | |
| 9468 | 1 | H45014 | ESTs | |
| 29469 | 1 | H62829 | EST - RC_H62829 | |
| 18121 | 1 | AA191310 | Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 85) beta isoform | |
| 14705 | 1 | D59362 | EST - RC_D59362 | |
| 16692 | 1 | F04444 | ESTs | |
| 16543 | 1 | AA029430 | Hs.61557 EST | |
| 16359 | 1 | AA019197 | Hs.40763 ESTs | |
| 40818 | 1 | N83772 | Hs.14550 Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydro | |
| 35205 | 1 | AA398161 | Hs.97602 ESTs | |
| 17794 | 1 | AA249175 | Hs.96334 ESTs Weakly similar to GOLIATH PROTEIN [Drosophila melanogaster] | |
| 11347 | 1 | AA150260 | Hs.72062 EST | |
| 17919 | 1 | AA224245 | Hs.28612 ESTs | |
| 22184 | 1 | AA161125 | Hs.72384 EST | |
| 14827 | 1 | R53520 | Hs.102755 ESTs | |
| 28091 | 1 | T35286 | Hs.90421 ESTs | |
| 28815 | 1 | AA481788 | Hs.87593 ESTs | |
| 24655 | 1 | D59267 | Hs.56762 ESTs | |
| 15611 | 1 | AA151480 | Hs.91202 ESTs | |
| 39998 | 1 | Z39151 | ESTs Weakly similar to Lpin17p [S. cerevisiae] | |
| 15700 | 1 | V51743 | Hs.35096 ESTs | |
| 22045 | 1 | H62965 | Hs.38132 ESTs | |
| 36770 | 1 | W73859 | Hs.78061 Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds | |
| 9877 | 1 | R48055 | Hs.24796 EST | |
| 22467 | 1 | AA435753 | EST - RC_AA435753 | |
| | 1 | N31127 | ESTs | |
| | 1 | R68284 | Hs.26399 ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-------------------|---|--|
| 32400 | 1 | R9/176 | Hs.110783 | ESTs | |
| 10602 | 1 | AA069425 | Hs.20573 | ESTs | |
| 23033 | 1 | T17353 | Hs.108894 | Human sapiens clone 23918 mRNA sequence | |
| 17593 | 1 | AA129856 | EST - RC_AA129856 | EST | |
| 14967 | 1 | T58588 | Hs.100419 | ESTs | |
| 20266 | 1 | N32118 | Hs.107385 | ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens] | |
| 14447 | 1 | AA069045 | Hs.11759 | ESTs | |
| 37994 | 1 | AA479919 | EST - RC_AA479919 | EST | |
| 12892 | 1 | AA426521 | Hs.18528 | Human sapiens mRNA for NA14 protein | |
| 11970 | 1 | AA280087 | Hs.4069 | ESTs | |
| 16738 | 1 | H53059 | Hs.15548 | ESTs | |
| 14471 | 1 | AA609346 | Hs.20102 | ESTs | |
| 14855 | 1 | T54752 | Hs.9786 | ESTs | |
| 24725 | 1 | Z39781 | Hs.8004 | Human sapiens Duo mRNA complete cds | |
| 5796 | 1 | X55019 | Hs.99975 | Cholergic receptor nicotinic delta polypeptide | |
| 20259 | 1 | N31598 | Hs.12727 | ESTs | |
| 18441 | 1 | AA232508 | Hs.77480 | ESTs | |
| 18458 | 1 | AA233177 | Hs.87134 | ESTs | |
| 10184 | 1 | R47433 | Hs.19400 | ESTs Weakly similar to MITOTIC MA22 PROTEIN [S.cerevisiae] | |
| 8830 | 1 | AB002319 | Hs.8653 | Human mRNA for KIAA0321 gene partial cds | |
| 15287 | 1 | V07461 | Hs.121559 | ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae] | |
| 18477 | 1 | AA026031 | Hs.64312 | ESTs | |
| 21969 | 1 | R45334 | Hs.21175 | ESTs | |
| 22340 | 1 | R41522 | Hs.25892 | ESTs | |
| 12894 | 1 | AA192569 | EST - RC_AA426259 | EST | |
| 6862 | 1 | AA477691 | Hs.104476 | ESTs | |
| 22594 | 1 | R79753 | Hs.23900 | ESTs | |
| 19131 | 1 | H03301 | Hs.122791 | ESTs | |
| 17103 | 1 | AA074597 | EST - RC_AA074597 | EST | |
| 35020 | 1 | AA402493 | Hs.10552 | ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus] | |
| 35401 | 1 | AA369593 | Hs.97692 | EST | |
| 10901 | 1 | AA112307 | Hs.25224 | ESTs | |
| 19546 | 1 | H07301 | Hs.32705 | ESTs | |
| 15378 | 1 | W26448 | Hs.15071 | ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus] | |
| 30292 | 1 | N35978 | Hs.82364 | ESTs | |
| 39087 | 1 | AA020697 | Hs.111591 | ESTs | |
| 37996 | 1 | AA077463 | Hs.77039 | Ribosomal protein S28 | |
| 8836 | 1 | AB002325 | Hs.105917 | Human mRNA for KIAA0327 protein complete cds | |
| 16150 | 1 | AA005428 | Hs.60140 | ESTs | |
| 23955 | 1 | T07467 | Hs.18065 | ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens] | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------|--|--|
| 37612 | 1 | AA489339 | Hs.105323 | ESTs | |
| 14782 | 1 | S72370 | Hs.85900 | Pyruvate carboxylase | |
| 23540 | 1 | T91878 | Hs.14463 | ESTs | |
| 41552 | 1 | R59332 | Hs.101253 | Human mRNA for KIAA0296 gene complete cds | |
| 21836 | 1 | R42569 | Hs.22444 | EST | |
| 11467 | 1 | AA234089 | Hs.14593 | ESTs | |
| 18347 | 1 | AA219230 | Hs.14593 | ESTs | |
| 8215 | 1 | AA369673 | Hs.84344 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 15505 | 1 | W26366 | Hs.7252 | Homo sapiens clone 24800 mRNA sequence | |
| 22784 | 1 | F93802 | Hs.33687 | ESTs | |
| 14966 | 1 | U07620 | Hs.89661 | Human MAP kinase mRNA complete cds | |
| 24213 | 1 | W69184 | Hs.23973 | ESTs | |
| 8165 | 1 | AA369888 | Hs.104135 | Homo sapiens mRNA for DRIM protein | |
| 32724 | 1 | T91750 | Hs.15230 | ESTs Weakly similar to F2BP2.2 [C.elegans] | |
| 8212 | 1 | AA386236 | Hs.96757 | Homo sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds | |
| 9834 | 1 | M92269 | Hs.22554 | Homo box BS (2.1 protein) | |
| 7229 | 1 | AA052213 | Hs.81868 | ESTs | |
| 15849 | 1 | Y059725 | Hs.75074 | H.sapiens mRNA for MAP kinase activated protein kinase | |
| 42706 | 1 | T95538 | Hs.45060 | Human K+ channel beta 1a subunit mRNA alternatively spliced complete cds | |
| 9159 | 1 | D31463 | Hs.30062 | Homo sapiens clone 23505 unknown mRNA partial cde | |
| 20040 | 1 | H96712 | Hs.125198 | ESTs | |
| 42218 | 1 | T68444 | Hs.110095 | ESTs | |
| 15326 | 1 | W29730 | Hs.8124 | ESTs | |
| 17780 | 1 | AA150162 | Hs.42262 | ESTs Weakly similar to HYPOTHETICAL B8.1 KO PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans] | |
| 17595 | 1 | AA126529 | Hs.71166 | EST | |
| 31314 | 1 | N68996 | Hs.49278 | EST | |
| 9777 | 1 | M57688 | Hs.90946 | GRANZYME H PRECURSOR | |
| 15373 | 1 | W25376 | Hs.74563 | THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR | |
| 23547 | 1 | T78448 | Hs.14577 | EST | |
| 12076 | 1 | AA284362 | Hs.6448 | ESTs Weakly similar to No definition line found [C.elegans] | |
| 11956 | 1 | AA270591 | Hs.124691 | ESTs | |
| 15391 | 1 | W29651 | Hs.15961 | ESTs | |
| 9287 | 1 | D62557 | Hs.18104 | ESTs | |
| 18419 | 1 | AA022466 | Hs.61141 | EST | |
| 21713 | 1 | R39530 | Hs.21034 | ESTs | |
| 12905 | 1 | AA427537 | Hs.32419 | ESTs | |
| 30257 | 1 | N34961 | Hs.75873 | H.sapiens mRNA for Zyrin | |
| 28134 | 1 | AA487622 | Hs.64095 | ESTs | |
| 16390 | 1 | AA019750 | Hs.40797 | ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens] | |
| 10553 | 1 | AA028504 | Hs.33215 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------------|--|--|
| 18063 | 1 | AA180054 | Hs.73677 | ESTs | |
| 39620 | 1 | H24085 | Hs.25443 | ESTs | |
| 7374 | 1 | AA093378 | Hs.101810 | ESTs | |
| 13109 | 1 | AA435688 | Hs.7995 | ESTs | |
| 19378 | 1 | H19673 | Hs.31670 | ESTs | |
| 24325 | 1 | W94733 | Hs.3978 | ESTs | |
| 22318 | 1 | R60224 | Hs.7095 | ESTs | |
| 24249 | 1 | W73059 | Hs.12600 | ESTs | |
| 16514 | 1 | AA102946 | Hs.44608 | ESTs | |
| 21431 | 1 | R21741 | Hs.23258 | EST | |
| 8397 | 1 | AA405178 | Hs.71125 | ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens] | |
| 8412 | 1 | AA426090 | Hs.26102 | ESTs | |
| 10072 | 1 | R14782 | Hs.31931 | ESTs | |
| 10349 | 1 | AA001898 | Hs.10160 | ESTs | |
| 14462 | 1 | AA036635 | Hs.27497 | ESTs | |
| 14830 | 1 | T92512 | EST - T92512 | | |
| 15851 | 1 | X81001 | Hs.141503 | Small inducible cytokine A5 (RANTES) | |
| 15706 | 1 | AA043800 | Hs.62645 | ESTs | |
| 16744 | 1 | AA045643 | Hs.62666 | ESTs | |
| 16950 | 1 | AA062980 | Hs.66990 | ESTs | |
| 17636 | 1 | AA185779 | Hs.29759 | ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens] | |
| 18634 | 1 | F10207 | Hs.13269 | ESTs | |
| 19178 | 1 | H10592 | Hs.100910 | EST | |
| 19757 | 1 | H54720 | Hs.35941 | ESTs | |
| 21341 | 1 | R14959 | Hs.21871 | EST Moderately similar to ntsein [M.musculus] | |
| 21466 | 1 | R24518 | Hs.23674 | EST | |
| 21602 | 1 | R36624 | Hs.135137 | ESTs | |
| 21748 | 1 | R40697 | Hs.21290 | EST | |
| 21860 | 1 | R43069 | EST - RC_R43069 | | |
| 21891 | 1 | R43590 | Hs.13290 | ESTs | |
| 21937 | 1 | R44508 | Hs.22653 | ESTs | |
| 22006 | 1 | R46244 | Hs.23110 | ESTs | |
| 22054 | 1 | R40116 | Hs.25067 | EST | |
| 22222 | 1 | R55042 | Hs.106645 | ESTs | |
| 22292 | 1 | R59385 | Hs.141035 | Homo sapiens basophilin (VMD2) mRNA alternatively spliced product complete cds | |
| 22363 | 1 | R63463 | Hs.23282 | ESTs | |
| 22446 | 1 | R67259 | Hs.25998 | EST | |
| 23103 | 1 | T23939 | Hs.7344 | ESTs | |
| 23872 | 1 | T94562 | Hs.17338 | EST | |
| 24291 | 1 | V80042 | Hs.10691 | ESTs | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|--------------|---|--|
| 24640 | 1 | Z39006 | Hs.21403 | ESTs | |
| 27519 | 1 | AA435935 | Hs.9695 | ESTs | |
| 32087 | 1 | RG4424 | Hs.64896 | ESTs | |
| 32294 | 1 | RA4210 | Hs.91440 | EST | |
| 32692 | 1 | T75942 | Hs.96500 | ESTs | |
| 37114 | 1 | Z39430 | Hs.65749 | ESTs | |
| 37333 | 1 | Z39668 | Hs.65792 | ESTs | |
| 37373 | 1 | AFFX- | AFFX-DapK-3 | | |
| 3873 | 1 | AA400034 | Hs.97769 | EST | |
| 35434 | 1 | AA412468 | Hs.104778 | ESTs | |
| 35950 | 1 | AA428865 | Hs.98563 | EST | |
| 36463 | 1 | AA431469 | Hs.98737 | ESTs | |
| 36615 | 1 | AA452138 | Hs.3761 | Homo sapiens BAC clone RG11BD07 from 7431 | |
| 37329 | 1 | AA461050 | Hs.124626 | EST | |
| 37700 | 1 | AA489940 | Hs.105302 | ESTs | |
| 38285 | 1 | AA609422 | Hs.112705 | EST | |
| 38887 | 1 | AA609606 | Hs.112732 | ESTs | |
| 38933 | 1 | H42037 | Hs.144150 | ESTs | |
| 39894 | 1 | H91680 | Hs.30250 | Homo sapiens short form transcription factor C/MAF (c-maf) mRNA complete cds | |
| 40244 | 1 | N47562 | Hs.102624 | EST | |
| 40545 | 1 | N63787 | Hs.109304 | ESTs | |
| 40819 | 1 | R45611 | Hs.137696 | ESTs Weakly similar to IIII ALL SUBFAMILY SO WARNING ENTRY IIII [H.sapiens] | |
| 41445 | 1 | R65829 | Hs.101883 | EST | |
| 41700 | 1 | T03170 | Hs.100165 | EST | |
| 41776 | 1 | AA446587 | Hs.6775 | ESTs Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens] | |
| 13254 | 1 | AA362708 | Hs.5009 | ESTs Weakly similar to mTERF [H.sapiens] | |
| 8171 | 1 | T17291 | Hs.6995 | ESTs | |
| 23030 | 1 | AA427510 | Hs.104287 | ESTs | |
| 8406 | 1 | AA046650 | Hs.40342 | ESTs | |
| 16767 | 1 | AA005315 | Hs.51262 | ESTs | |
| 25010 | 1 | T35529 | EST - T35529 | | |
| 14829 | 1 | AA280634 | Hs.132872 | ESTs Moderately similar to IIII ALL SUBFAMILY SC WARNING ENTRY IIII [H.sapiens] | |
| 34584 | 1 | Y07868 | Hs.38842 | H.sapiens mRNA for Plrin isolate 1 | |
| 15909 | 1 | N44971 | Hs.107164 | Scenedes beta non-cyathocycle 1 | |
| 9622 | 1 | W26408 | Hs.107726 | ESTs Weakly similar to LIS-1 protein [H.sapiens] | |
| 15361 | 1 | RG3024 | Hs.25945 | ESTs | |
| 22169 | 1 | AA352762 | Hs.31235 | ESTs | |
| 11690 | 1 | T16510 | Hs.6624 | ESTs | |
| 22895 | 1 | Z38153 | Hs.26521 | ESTs | |
| 24490 | 1 | H91255 | Hs.15227 | ESTs | |
| 19593 | 1 | | | | |

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FIGURE 7 (CONT.)

| | | | | | |
|-------|---|----------|-----------|---|--|
| 10690 | 1 | H48825 | Hs.36291 | ESTs | |
| 12450 | 1 | AA401509 | Hs.15955 | ESTs | |
| 24368 | 1 | W87280 | Hs.124800 | ESTs | |
| 22585 | 1 | R77631 | Hs.29126 | ESTs | |
| 18872 | 1 | F10542 | Hs.12292 | ESTs | |
| 15358 | 1 | V026105 | Hs.8991 | ESTs | |
| 24186 | 1 | W61319 | Hs.37482 | ESTs Highly similar to COATLIMER ZETA SUBUNIT [Bos taurus] | |
| 23863 | 1 | T03078 | Hs.17255 | ESTs | |
| 23846 | 1 | T03078 | Hs.17117 | ESTs | |
| 15143 | 1 | U79257 | Hs.89821 | Human clone 23932 mRNA sequence | |
| 9711 | 1 | L4334 | Hs.10432 | ESTs Weakly similar to BENZYLGLUTAMATE RESISTANCE PROTEIN [Candida albicans] | |
| 22844 | 1 | R74233 | Hs.50844 | Human sapiens mRNA for RIA0573 protein partial cds | |
| 41506 | 1 | R2088 | | EST - RC_R52088 | |
| 39345 | 1 | C21105 | Hs.7768 | Human sapiens FGF-1 intracellular binding protein (FIBP) mRNA complete cds | |
| 22772 | 1 | R39522 | Hs.25590 | ESTs | |
| 16434 | 1 | AA024694 | Hs.61199 | EST - RC_AA084412 | |
| 17255 | 1 | AA094412 | | EST - RC_AA084412 | |
| 22692 | 1 | R87711 | Hs.34183 | ESTs | |
| 38830 | 1 | AA069189 | Hs.116415 | ESTs | |
| 9179 | 1 | D50312 | Hs.102308 | Human mRNA for ukATP-1 complete cds | |
| 42547 | 1 | W73548 | | EST - RC_W73548 | |
| 36195 | 1 | AA421144 | | EST - RC_AA421144 | |
| 29355 | 1 | H70121 | Hs.79592 | ESTs | |
| 34608 | 1 | AA281765 | Hs.104441 | ESTs | |
| 20779 | 1 | N67563 | Hs.18917 | ESTs | |
| 11081 | 1 | AA148826 | Hs.34274 | ESTs | |
| 12151 | 1 | AA301269 | Hs.24642 | ESTs | |
| 39935 | 1 | H52379 | | EST - RC_H52379 | |
| 7157 | 1 | AA037199 | Hs.9939 | ESTs | |
| 17658 | 1 | AA156596 | Hs.72146 | ESTs | |
| 34893 | 1 | AA302831 | Hs.57732 | Human sapiens p38beta2 MAP kinase mRNA complete cds | |
| 18445 | 1 | AA332648 | Hs.87058 | ESTs | |
| 22524 | 1 | R72597 | | EST - RC_R72597 | |
| 19224 | 1 | H12448 | Hs.124570 | ESTs Weakly similar to unknown protein [H sapiens] | |
| 18803 | 1 | F09988 | Hs.5244 | ESTs | |
| 13810 | 1 | AA464689 | Hs.23294 | ESTs Weakly similar to weak similarity to HSP90 [C. elegans] | |
| 18070 | 1 | AA180352 | Hs.72733 | ESTs | |
| 17937 | 1 | AA164750 | Hs.72499 | ESTs | |
| 39115 | 1 | AA620736 | Hs.112893 | EST | |
| 22517 | 1 | R71892 | Hs.25986 | ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Carica porcellus] | |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-------------------|--|
| 16906 | 1 | AA059555 | Hs.63392 | EST |
| 14251 | 1 | AAJ97049 | Hs.32501 | ESTs |
| 23923 | 1 | T98407 | Hs.17812 | ESTs |
| 21177 | 1 | R09569 | Hs.19721 | ESTs |
| 23705 | 1 | AA131024 | Hs.71030 | ESTs |
| 19805 | 1 | H07725 | Hs.124031 | ESTs |
| 19988 | 1 | H47866 | Hs.33991 | EST |
| 36693 | 1 | AA432389 | Hs.98702 | ESTs |
| 14036 | 1 | AA482407 | Hs.5473 | ESTs |
| 20869 | 1 | N98645 | Hs.10702 | ESTs |
| 23849 | 1 | T33113 | EST - RC_T93113 | |
| 18265 | 1 | AA207122 | Hs.86316 | ESTs |
| 33275 | 1 | AA398530 | Hs.97363 | ESTs |
| 10262 | 1 | R77869 | Hs.110453 | ESTs |
| 21757 | 1 | R40789 | Hs.21299 | ESTs |
| 21541 | 1 | R31607 | Hs.24420 | ESTs |
| 18873 | 1 | AA055258 | Hs.63264 | EST |
| 19646 | 1 | I46006 | Hs.31677 | ESTs |
| 23719 | 1 | T89180 | Hs.138506 | ESTs |
| 19608 | 1 | H41581 | Hs.31562 | ESTs Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans] |
| 17382 | 1 | AA102731 | Hs.103072 | ESTs |
| 18864 | 1 | AA055971 | Hs.63238 | ESTs |
| 10897 | 1 | AA111881 | Hs.9192 | ESTs |
| 17028 | 1 | AA070178 | EST - RC_AA070178 | |
| 19220 | 1 | H12318 | Hs.24324 | ESTs |
| 9726 | 1 | L44574 | Hs.125235 | ESTs |
| 24570 | 0 | Z38681 | Hs.27150 | ESTs |
| 22167 | 0 | R53021 | Hs.25873 | ESTs |
| 42537 | 0 | W73417 | Hs.103183 | EST |
| 18806 | 0 | F10005 | Hs.12599 | ESTs |
| 16585 | 0 | AA033548 | Hs.4236 | ESTs |
| 17309 | 0 | AA086232 | Hs.68717 | EST Moderately similar to maninrin transposase [H.sapiens] |
| 22813 | 0 | R97419 | Hs.35718 | ESTs |
| 18429 | 0 | AA022953 | Hs.61172 | EST |
| 22013 | 0 | R46526 | Hs.26377 | EST |
| 8439 | 0 | AA431277 | Hs.32419 | ESTs |
| 22934 | 0 | T10042 | Hs.4205 | ESTs |
| 13063 | 0 | AA432386 | Hs.1191 | Human mRNA for KIAA0073 gene partial cds |
| 10122 | 0 | R31745 | EST - R31745 | |
| 18195 | 0 | AA195263 | Hs.89001 | EST |

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FIGURE 7 (CONT.)

| | | | | |
|-------|---|----------|-------------------|---------------------------------|
| 33249 | 0 | W72557 | Hs 57836 | ESTs |
| 15956 | 0 | AA063378 | Hs 144270 | ESTs |
| 15953 | 0 | AA223929 | Hs 89902 | EST |
| 34154 | 0 | AA219304 | Hs 74561 | ALPHA-2-MACROGLOBULIN PRECURSOR |
| 16222 | 0 | AA011210 | Hs 95044 | ESTs |
| 17174 | 0 | AA079306 | EST - RC_AA079306 | |

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| Primary Key | fold upregulated of Tumor over normal cells | Accession | Unigene Descriptor | ORF structural info |
|-------------|---|-----------|--|---------------------|
| 16074 | >10 | AA001507 | ESTs | other |
| 25047 | >10 | AA011031 | ESTs | other |
| 25082 | >10 | AA017257 | ESTs | other |
| 16490 | >10 | AA026418 | ESTs | other |
| 25179 | >10 | AA031268 | H sapiens mRNA for kinesin-2 | other |
| 25215 | >10 | AA035540 | APOLIPOPROTEIN AI REGULATORY PROTEIN-1 | other |
| 25282 | >10 | AA044825 | ESTs | other |
| 16810 | >10 | AA053636 | ESTs | other |
| 16835 | >10 | AA054438 | ESTs | SS. |
| 10747 | >10 | AA055841 | ESTs | other |
| 10748 | >10 | AA055892 | ESTs | other |
| 16693 | >10 | AA055300 | Human mRNA for KIAA0035 gene partial cds | other |
| 17051 | >10 | AA070801 | ESTs | TM |
| 10840 | >10 | AA084104 | ESTs | other |
| 7296 | >10 | AA085661 | ESTs | other |
| 7325 | >10 | AA090842 | ESTs Weakly similar to HYPOTHETICAL 35.7 KD PROTEIN C27F 02G IN CHROMOSOME 1 [Schistosoma mansoni] | other |
| 17419 | >10 | AA113349 | EST | ? |
| 17541 | >10 | AA127459 | ESTs | other |
| 17559 | >10 | AA128407 | ESTs | other |
| 25609 | >10 | AA128978 | ESTs | ? |
| 17600 | >10 | AA130596 | ESTs | other |
| 10992 | >10 | AA132523 | Homo sapiens BAC clone RG119C02 from 7p15 | other |
| 17654 | >10 | AA133250 | ESTs | TM |
| 17734 | >10 | AA137248 | ESTs | other |
| 25801 | >10 | AA148530 | EST - RC_AA148530 | TM |
| 25806 | >10 | AA149007 | EST | ? |
| 11121 | >10 | AA156359 | Human TAR DNA-binding protein-43 mRNA complete cds | ? |
| 11150 | >10 | AA164289 | ESTs | other |
| 25625 | >10 | AA164494 | ESTs Weakly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (H.sapiens) | other |
| 25934 | >10 | AA165335 | Human clone ccds unknown protein mRNA complete cds | ? |
| 17987 | >10 | AA169379 | ESTs | other |
| 16008 | >10 | AA171895 | Homo sapiens clone 24749 end 24750 mRNA sequences | TM |
| 33953 | >10 | AA173290 | Human HOXA1 mRNA long transcript and alternatively spliced forms complete cds | other |
| 33980 | >10 | AA190223 | CAMP-DEPENDENT PROTEIN KINASE TYPE II: ALPHA REGULATORY CHAIN | other |
| 34013 | >10 | AA190888 | EST - RC_AA190888 | other |
| 34014 | >10 | AA191346 | ESTs | other |
| 34015 | >10 | AA191353 | ESTs | TM |
| 34070 | >10 | AA195549 | ESTs | other |
| 18260 | >10 | AA206601 | ESTs | ? |
| 34105 | >10 | AA207123 | ESTs | SS. |
| 34107 | >10 | AA209469 | ESTs | other |
| 18330 | >10 | AA216722 | Human mRNA for apolipoprotein E receptor 2 complete cds | TM |
| 16362 | >10 | AA223912 | Ribonuclease L (2'5'-oligoadenylate synthetase- dependent) inhibitor | other |
| 18392 | >10 | AA227751 | ESTs | SS. |
| 34188 | >10 | AA228030 | ESTs | TM |
| 34197 | >10 | AA232315 | Homo sapiens clone 23767 and 23917 mRNA partial cds | other |
| 25048 | >10 | AA234365 | Homo sapiens survival of motor neuron protein interacting protein 1 (SP1) mRNA complete cds | ? |
| 25951 | >10 | AA234556 | EST | ? |

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| | | | | |
|-------|-----|----------|--|-------|
| 11561 | >10 | AA236033 | Ev-1 | other |
| 20059 | >10 | AA236685 | ESTs | other |
| 26100 | >10 | AA242835 | Human mRNA for KIAA0391 gene complete cds | other |
| 11663 | >10 | AA243052 | ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus] | other |
| 7785 | >10 | AA243375 | EST - AA243375 | other |
| 34372 | >10 | AA251973 | ESTs | ? |
| 26240 | >10 | AA252282 | Human mRNA for KIAA0152 gene complete cds | TM |
| 34362 | >10 | AA252512 | ESTs | other |
| 34391 | >10 | AA252703 | EST - RC_AA252703 | other |
| 26274 | >10 | AA253011 | ESTs | ? |
| 34400 | >10 | AA253400 | ESTs | other |
| 26291 | >10 | AA253422 | ESTs | ? |
| 26355 | >10 | AA256379 | ESTs | other |
| 11813 | >10 | AA256858 | ESTs | other |
| 34518 | >10 | AA278721 | ESTs | ? |
| 26545 | >10 | AA278979 | ESTs | other |
| 26574 | >10 | AA279504 | ESTs | other |
| 34554 | >10 | AA280015 | DNA polymerase gamma | other |
| 34561 | >10 | AA280098 | ESTs | TM |
| 26628 | >10 | AA280641 | ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus] | TM |
| 11969 | >10 | AA280670 | ESTs | SS. |
| 34575 | >10 | AA280738 | ESTs | TM |
| 26677 | >10 | AA281636 | ESTs | ? |
| 26700 | >10 | AA282197 | EST | ? |
| 34672 | >10 | AA284372 | ESTs | other |
| 34692 | >10 | AA285079 | ESTs | other |
| 12143 | >10 | AA290991 | ESTs | other |
| 6092 | >10 | AA316272 | ESTs | TM |
| 34904 | >10 | AA321748 | EST | other |
| 8111 | >10 | AA323787 | ESTs | other |
| 8125 | >10 | AA330771 | Human protein-tyrosine phosphatase (SH-PTP-1) mRNA partial sequence | TM |
| 26916 | >10 | AA331393 | ESTs | other |
| 26926 | >10 | AA342402 | ESTs | other |
| 26935 | >10 | AA347193 | ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans] | TM |
| 35038 | >10 | AA350541 | ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H sapiens] | TM |
| 35049 | >10 | AA350857 | ESTs | other |
| 35106 | >10 | AA371561 | EST Weakly similar to putative p150 [H sapiens] | ? |
| 35197 | >10 | AA388120 | ESTs | other |
| 35277 | >10 | AA398536 | ESTs | other |
| 35309 | >10 | AA399000 | EST | other |
| 35322 | >10 | AA398710 | H sapiens RNA for CLC3 | TM |
| 27007 | >10 | AA400198 | ESTs | TM |
| 35495 | >10 | AA400627 | ESTs | ? |
| 27046 | >10 | AA400670 | Homo sapiens mRNA for KIAA0552 protein partial cds | other |
| 35500 | >10 | AA400715 | ESTs | other |
| 12480 | >10 | AA402116 | Homo sapiens U-mRNP-associated cyclophilin (USA-Cy7) mRNA complete cds | other |
| 35693 | >10 | AA405485 | ESTs Weakly similar to similar to t complex testis-specific protein [C elegans] | other |
| 35697 | >10 | AA405512 | ESTs | other |
| 35766 | >10 | AA406169 | Homo sapiens KIAA0431 mRNA partial cds | other |
| 35769 | >10 | AA406206 | ESTs | other |
| 35798 | >10 | AA410031 | ESTs | other |

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| | | | | |
|-------|-----|----------|--|--------|
| 35801 | >10 | AA410291 | ESTs | other |
| 35803 | >10 | AA410295 | ESTs | other |
| 35822 | >10 | AA411144 | ESTs | TM |
| 35874 | >10 | AA412024 | EST | ? |
| 35858 | >10 | AA412550 | ESTs | other |
| 36052 | >10 | AA417027 | EST | TM |
| 36258 | >10 | AA423062 | ESTs Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY H ¹ (H sapiens) | other |
| 36288 | >10 | AA424502 | ESTs | other |
| 36307 | >10 | AA424803 | EST | ? |
| 36371 | >10 | AA426017 | ESTs | TM |
| 36395 | >10 | AA426353 | ESTs | other |
| 36405 | >10 | AA426406 | Homo sapiens mRNA for KIAA0630 protein partial cds | other |
| 36506 | >10 | AA429610 | ESTs | other |
| 36571 | >10 | AA430726 | EST - RC_AA430726 | SS |
| 36695 | >10 | AA433910 | ESTs | other |
| 36739 | >10 | AA435610 | EST - RC_AA435610 | ? |
| 36753 | >10 | AA435686 | ESTs | other |
| 36845 | >10 | AA436196 | ESTs | ? |
| 13136 | >10 | AA436560 | ESTs | SS, TM |
| 13143 | >10 | AA436619 | ESTs | SS |
| 36868 | >10 | AA442060 | ESTs | other |
| 36962 | >10 | AA442062 | ESTs | ? |
| 36961 | >10 | AA442845 | EST | ? |
| 13237 | >10 | AA443971 | ESTs Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY H ¹ (H sapiens) | ? |
| 13242 | >10 | AA445994 | ESTs | other |
| 37057 | >10 | AA446131 | ESTs | other |
| 37066 | >10 | AA446312 | ESTs Weakly similar to H ¹ ALU CLASS C WARNING ENTRY H ¹ (H sapiens) | other |
| 37074 | >10 | AA446344 | ESTs | SS |
| 37064 | >10 | AA446486 | Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds | ? |
| 37135 | >10 | AA447540 | EST | ? |
| 37159 | >10 | AA447714 | EST - RC_AA447714 | other |
| 37168 | >10 | AA447772 | ESTs | ? |
| 37246 | >10 | AA449311 | Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds | other |
| 37310 | >10 | AA451707 | ESTs | other |
| 37453 | >10 | AA454610 | ESTs | ? |
| 37456 | >10 | AA454632 | ESTs | TM |
| 27787 | >10 | AA454660 | ESTs | ? |
| 37492 | >10 | AA455246 | EST - RC_AA455246 | other |
| 37546 | >10 | AA455641 | ESTs | TM |
| 37601 | >10 | AA458064 | ESTs | other |
| 37611 | >10 | AA459396 | Human signaling lymphocyte activation molecule (SLAM) mRNA complete cds | SS, TM |
| 37615 | >10 | AA459101 | Human serine/threonine kinase mRNA partial cds | other |
| 37653 | >10 | AA460017 | ESTs | other |
| 37677 | >10 | AA460030 | Homo sapiens orphan G protein-coupled receptor HGC30 mRNA complete cds | other |
| 37777 | >10 | AA464860 | Homo sapiens jak2 kinase mRNA complete cds | other |
| 6648 | >10 | AA465016 | Homo sapiens serine protease-like protease (hes1) mRNA complete cds | ? |
| 37816 | >10 | AA469954 | EST | ? |
| 37829 | >10 | AA470084 | ESTs | other |
| 28015 | >10 | AA477421 | ESTs | other |
| 37978 | >10 | AA479294 | EST - RC_AA479294 | other |
| 37979 | >10 | AA479295 | ESTs Highly similar to RING CANAL PROTEIN [Drosophila melanogaster] | other |

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| | | | | |
|-------|-----|---------------------------|--|-------|
| 37953 | >10 | AA479348 | H sapiens mRNA for SYT | other |
| 14054 | >10 | AA485223 | ESTs | TM |
| 38121 | >10 | AA485724 | EST - RC_AA485724 | other |
| 28122 | >10 | AA485928 | ESTs Weakly similar to LOK (H musculus) | other |
| 38167 | >10 | AA487207 | EST - RC_AA487207 | other |
| 38172 | >10 | AA487424 | EST - RC_AA487424 | other |
| 38179 | >10 | AA487492 | Human sapiens clone 23592 mRNA sequence | other |
| 38182 | >10 | AA487501 | ESTs | other |
| 38194 | >10 | AA487969 | ESTs | other |
| 28141 | >10 | AA488432 | ESTs | ? |
| 38211 | >10 | AA488687 | ESTs | other |
| 38235 | >10 | AA489020 | ESTs | other |
| 38280 | >10 | AA489791 | EST - RC_AA489791 | other |
| 38316 | >10 | AA490500 | Human sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds | other |
| 38330 | >10 | AA490682 | ESTs | other |
| 38456 | >10 | AA504342 | ESTs | SS |
| 38480 | >10 | AA504402 | ESTs | other |
| 38553 | >10 | AA521471 | ESTs | other |
| 38580 | >10 | AA596545 | ESTs | ? |
| 38590 | >10 | AA596646 | Human mRNA for transcriptional activator hSNF2b complete cds | other |
| 38601 | >10 | AA596736 | ESTs | ? |
| 28323 | >10 | AA599639 | ESTs | other |
| 38828 | >10 | AA609177 | ESTs | TM |
| 38838 | >10 | AA609215 | EST - RC_AA609215 | ? |
| 38867 | >10 | AA609318 | Human cdk-6 mRNA complete cds | TM |
| 38871 | >10 | AA609332 | EST | ? |
| 38970 | >10 | AA609749 | ESTs | other |
| 38994 | >10 | AA609829 | ESTs Moderately similar to Hs ALU SUBFAMILY J WARNING ENTRY III (H sapiens) | ? |
| 39045 | >10 | AA610077 | ESTs | other |
| 39062 | >10 | AA620332 | EST | ? |
| 39080 | >10 | AA620552 | EST - RC_AA620552_r | ? |
| 39110 | >10 | AA670709 | ESTs Weakly similar to HYPOTHEtical 90 K D PROTEIN TOSH10.7 IN CHROMOSOME II (C elegans) | other |
| 39176 | >10 | AA671091 | ESTs | other |
| 39218 | >10 | AA671330 | ESTs | other |
| 39221 | >10 | AA671340 | Human sapiens protein phosphatase with EF-hands-1 (PPEF-1) mRNA complete cds | other |
| 39232 | >10 | AA671409 | ESTs | other |
| 21 | >10 | AB000905 | H sapiens histone H4 gene | ? |
| 6963 | >10 | AFFX- HUMTFRRM11507_M | AFFX-HUMTFRRM11507_M | ? |
| 33890 | >10 | AFFX- HUMTFRRM11507_D7 | AFFX-HUMTFRRM11507_5 | ? |
| 39302 | >10 | C14944 | ESTs | other |
| 39329 | >10 | C20797 | EST | ? |
| 28644 | >10 | D12163 | ESTs | other |
| 218 | >10 | D13540 | PROTEIN-TYROSINE PHOSPHATASE 2C | other |
| 236 | >10 | D13645 | Human mRNA for KIAA0020 gene complete cds | other |
| 9127 | >10 | D30027 | PHOSPHATIDYLINOSITOL | other |
| 459 | >10 | D36793 | Human mRNA for catrin-like protein complete cds | TM |
| 39405 | >10 | D50975 | ESTs | other |
| 39433 | >10 | D52027 | Human thymidine kinase 2 (TK2) mRNA complete cds | other |
| 39438 | >10 | D57692 | Human Ca2+-dependent activator protein for secretion mRNA complete cds | TM |
| 14708 | >10 | D59368 | EST | ? |

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| | | | | |
|-------|-----|---------------|--|--------|
| 39488 | >10 | D60831 | ESTs | other |
| 39504 | >10 | D60632 | ESTs | other |
| 765 | >10 | D65096 | Prostaglandin E receptor 3 (subtype EP3) (alternative products) | ? |
| 787 | >10 | D65969 | Human mRNA for KIAA0215 gene complete cds | other |
| 789 | >10 | D65971 | Human mRNA for KIAA0217 gene partial cds | other |
| 39529 | >10 | F02202 | ESTs | ? |
| 39535 | >10 | F02450 | ESTs Moderately similar to unknown protein [H sapiens] | TM |
| 18675 | >10 | F04022 | ESTs | other |
| 18718 | >10 | F04915 | ESTs | other |
| 18762 | >10 | F09458 | ESTs | other |
| 18782 | >10 | F09739 | ESTs | other |
| 25090 | >10 | F13655 | ESTs Moderately similar to the ALU SUBFAMILY SBI WARNING ENTRY !!! [H sapiens] | other |
| 19001 | >10 | H02890 | ESTs | other |
| 19164 | >10 | H10395 | EST | ? |
| 36725 | >10 | H11323 | ESTs | other |
| 19203 | >10 | H11593 | ESTs | other |
| 19328 | >10 | H17808 | ESTs | other |
| 19387 | >10 | H20128 | ESTs | ? |
| 39787 | >10 | H20131 | ESTs | SS |
| 19388 | >10 | H20165 | EST | ? |
| 39632 | >10 | H26279 | EST - RC_H26279 | other |
| 19591 | >10 | H40588 | ESTs | other |
| 29229 | >10 | H48459 | Human mRNA for KIAA0186 gene complete cds | other |
| 19727 | >10 | H52702 | ESTs | ? |
| 19787 | >10 | H59579 | ESTs | other |
| 39995 | >10 | H62474 | EST | SS, TM |
| 28331 | >10 | H65116 | ESTs | TM |
| 29344 | >10 | H68839 | EST | ? |
| 40054 | >10 | H72283 | Human mRNA for KIAA0265 gene partial cds | other |
| 40083 | >10 | H73486 | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 | other |
| 19949 | >10 | H76283 | ESTs | TM |
| 40204 | >10 | H86296 | EST - RC_H86296 | other |
| 29523 | >10 | H86353 | ESTs Weakly similar to line-1 protein ORF2 [H sapiens] | ? |
| 29551 | >10 | H90134 | ESTs | ? |
| 29645 | >10 | H95640 | ESTs | ? |
| 20057 | >10 | H98079 | ESTs | other |
| 976 | >10 | HQ2036-HT2090 | EST - HQ2036-HT2090 | ? |
| 1158 | >10 | HQ3344-HT3521 | EST - HQ3344-HT3521 | ? |
| 1210 | >10 | HQ37-HT37 | EST - HQ37-HT37 | ? |
| 1345 | >10 | HQ4716-HT5158 | EST - HQ4716-HT5158 | ? |
| 1349 | >10 | HQ4747-HT5195 | EST - HQ4747-HT5195 | ? |
| 1445 | >10 | JC3027 | MHC class I protein HLA-G | ? |
| 1570 | >10 | K01383 | EST - K01383 | ? |
| 1684 | >10 | L07541 | Replication factor C (activator 1) 3 (39kD) | other |
| 1852 | >10 | L17328 | Human FEZ2 mRNA partial cds | TM |
| 1856 | >10 | L18920 | MELANOMA-ASSOCIATED ANTIGEN 2 | ? |
| 1863 | >10 | L19161 | TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT | other |
| 2070 | >10 | L37378 | Homo sapiens guanylyl cyclase (RetGC-2) mRNA complete cds | SS, TM |
| 2123 | >10 | L40386 | Homo sapiens (clone K22/71) mRNA fragment | other |
| 2144 | >10 | L41349 | Phospholipase C beta 4 | SS |
| 9723 | >10 | L44547 | ESTs | other |
| 2188 | >10 | L47276 | EST - L47276 | other |

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| | | | | |
|-------|-----|--------|--|-------|
| 2343 | >10 | M15353 | Eukaryotic translation initiation factor 4E | other |
| 2627 | >10 | M29610 | Glycophorin E | TM |
| 2857 | >10 | M58597 | Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific) | TM |
| 3021 | >10 | M05941 | Protein tyrosine phosphatase non-receptor type 4 | other |
| 3163 | >10 | M84424 | Cathepsin E | ? |
| 3196 | >10 | M86917 | Oxytocin binding protein | other |
| 20088 | >10 | N20054 | ESTs Weakly similar to putative p150 [H sapiens] | ? |
| 29795 | >10 | N20641 | ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN-3 [Homo sapiens] | other |
| 40427 | >10 | N21147 | ESTs | other |
| 40444 | >10 | N22140 | ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplexes octocornatus] | TM |
| 29693 | >10 | N23003 | ESTs | other |
| 40498 | >10 | N26086 | Homo sapiens citrate synthase mRNA complete cds | SS |
| 40559 | >10 | N33024 | ESTs | SS |
| 30190 | >10 | N33264 | EST | ? |
| 30207 | >10 | N33920 | H sapiens mRNA for dioxiquin | other |
| 20304 | >10 | N34686 | Homo sapiens clone 239-15 mRNA sequence | ? |
| 20307 | >10 | N34830 | ESTs | other |
| 30265 | >10 | N35115 | ESTs | other |
| 40594 | >10 | N35388 | ESTs | other |
| 40604 | >10 | N38893 | Homo sapiens KIAA0428 mRNA complete cds | other |
| 40631 | >10 | N45124 | ESTs | other |
| 40660 | >10 | N49104 | NUCLEAR FACTOR RIP140 | other |
| 30610 | >10 | N50138 | EST | ? |
| 30617 | >10 | N50646 | ESTs | other |
| 30631 | >10 | N50807 | EST | ? |
| 30790 | >10 | N52835 | EST | ? |
| 20564 | >10 | N56443 | ESTs | TM |
| 40760 | >10 | N57627 | ESTs Weakly similar to ELL [H. musculus] | other |
| 30938 | >10 | N58561 | Cathepsin B | other |
| 20614 | >10 | N59230 | ESTs | SS |
| 20657 | >10 | N62889 | ESTs | other |
| 31136 | >10 | N63512 | ESTs Weakly similar to M01F14 [C. elegans] | TM |
| 40827 | >10 | N64051 | Homo sapiens Werner syndrome gene complete cds | other |
| 31310 | >10 | N66631 | EST | ? |
| 40876 | >10 | N67607 | Human Rho-associated coiled-coil containing protein kinase p16ROCK mRNA complete cds | other |
| 20791 | >10 | N68057 | Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds | ? |
| 40905 | >10 | N68738 | ESTs | other |
| 40911 | >10 | N69114 | H sapiens mRNA for orphan nuclear hormone receptor | other |
| 40913 | >10 | N69218 | ESTs | other |
| 31484 | >10 | N69466 | ESTs | other |
| 31619 | >10 | N73449 | ESTs | other |
| 41005 | >10 | N79516 | ESTs | TM |
| 31818 | >10 | N89774 | Homo sapiens mRNA for KIAA0292 gene partial cds | other |
| 31872 | >10 | N91109 | EST | other |
| 41040 | >10 | N91948 | ESTs | other |
| 31944 | >10 | N93193 | ESTs | other |
| 41065 | >10 | N93618 | ESTs | other |
| 32034 | >10 | N98020 | ESTs Moderately similar to DMR-ND PROTEIN [H sapiens] | other |
| 41107 | >10 | R01634 | ESTs | other |
| 41163 | >10 | R08176 | ESTs | other |
| 21238 | >10 | R08564 | Plasminogen-like protein | other |

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| | | | | |
|-------|-----|--------|--|--------|
| 21240 | >10 | R08613 | ESTs | other |
| 21412 | >10 | R20670 | ESTs | other |
| 21519 | >10 | R27975 | EST - RC_H27975 | other |
| 41361 | >10 | R42278 | H sapiens mRNA for TRES | ? |
| 37189 | >10 | R43183 | ESTs | TM |
| 32195 | >10 | R43471 | ESTs Weakly similar to ORF YOKU55w (S cerevisiae) | other |
| 21902 | >10 | R43822 | EST | ? |
| 21946 | >10 | R44707 | ESTs | TM |
| 22072 | >10 | R49406 | ESTs | ? |
| 32240 | >10 | R50976 | Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor | other |
| 32258 | >10 | R55623 | ESTs | other |
| 22258 | >10 | R56437 | ESTs | other |
| 22282 | >10 | R59197 | ESTs | other |
| 32277 | >10 | R61490 | Human mRNA for rod photoreceptor protein complete cds | other |
| 22372 | >10 | R62831 | EST | ? |
| 22400 | >10 | R64109 | ESTs | other |
| 41590 | >10 | R64129 | ESTs | other |
| 10233 | >10 | R71427 | ESTs Highly similar to PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC [Saccharomyces cerevisiae] | other |
| 41654 | >10 | R76437 | THROMBOXANE A SYNTHASE | TM |
| 22557 | >10 | R76722 | ESTs | other |
| 22576 | >10 | R79111 | ESTs | other |
| 22590 | >10 | R79777 | EST | ? |
| 41678 | >10 | R80675 | EST | ? |
| 41719 | >10 | R89260 | EST - RC_R89260 | other |
| 22780 | >10 | R96208 | ESTs | other |
| 41752 | >10 | R97063 | ESTs | other |
| 3375 | >10 | S50223 | HKR-T1 | other |
| 3406 | >10 | S55896 | SQUAMOUS CELL CARCINOMA ANTIGEN 1 | other |
| 3522 | >10 | S90267 | Spleen tyrosine kinase | other |
| 41793 | >10 | T03867 | ESTs | ? |
| 23196 | >10 | T40630 | ESTs Weakly similar to D0035.14 (C. elegans) | other |
| 23360 | >10 | T58531 | ESTs | other |
| 32635 | >10 | T61116 | ESTs | other |
| 42177 | >10 | T79786 | ESTs | ? |
| 23623 | >10 | T84047 | ESTs | ? |
| 23662 | >10 | T86674 | ESTs | other |
| 42242 | >10 | T89579 | Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds | other |
| 23759 | >10 | T90313 | ESTs | other |
| 23832 | >10 | T92018 | ESTs | other |
| 32740 | >10 | T92950 | ESTs | other |
| 42290 | >10 | T95105 | ESTs | ? |
| 3559 | >10 | U01157 | Glucagon-like peptide-1 receptor | SS, TM |
| 3559 | >10 | U04213 | Protease inhibitor 5 (maspin) | other |
| 3739 | >10 | U10690 | Human MAGE-5a antigen (MAGE5a) gene complete cds | ? |
| 3870 | >10 | U14518 | Centromere protein A (17kD) | other |
| 3913 | >10 | U16261 | Human MDA-7 (mda-7) mRNA complete cds | SS, |
| 4029 | >10 | U21090 | Human DNA polymerase delta small subunit mRNA complete cds | other |
| 4157 | >10 | U28811 | Human cyclin-rich fibroblast growth factor receptor (CRR-1) mRNA complete cds | other |
| 4178 | >10 | U30246 | Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds | TM |
| 15006 | >10 | U30246 | Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds | TM |

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| | | | | |
|-------|-----|--------|--|-------|
| 4193 | >10 | U31116 | Human beta-sarcoglycan A3b mRNA complete cds | TM |
| 4306 | >10 | U30798 | Homo sapiens platelet cG-PDE mRNA complete cds | TM |
| 4367 | >10 | U39817 | Blooms syndrome | other |
| 4386 | >10 | U40622 | DNA repair protein XRCC4 | other |
| 4388 | >10 | U40714 | Human tyrosyl-tRNA synthetase mRNA complete cds | other |
| 4455 | >10 | U43944 | MALATE OXIDOREDUCTASE | other |
| 4477 | >10 | U45880 | Human VAP-like protein ILP mRNA complete cds | other |
| 4680 | >10 | U55766 | Human Rev interacting protein Rip-1 mRNA complete cds | TM |
| 4702 | >10 | U57341 | EST - U57341 | other |
| 4713 | >10 | U57721 | Human L-lysine hydrolase mRNA complete cds | other |
| 4787 | >10 | U51145 | Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds | other |
| 4862 | >10 | U55437 | Human homeodomain-containing protein (HNF1) mRNA complete cds | ? |
| 4945 | >10 | U59108 | Homo sapiens mRNA for TRAF-5 complete cds | other |
| 4975 | >10 | U71006 | Human MEK5 mRNA complete cds | other |
| 4994 | >10 | U72514 | Human C2f mRNA complete cds | other |
| 5002 | >10 | U72761 | Human karyophann beta 3 mRNA complete cds | other |
| 5021 | >10 | U73124 | Human putative ATP/GTP-binding protein (HEA8) mRNA complete cds | TM |
| 5149 | >10 | U79716 | Human resin (RELN) mRNA complete cds | SS |
| 5214 | >10 | U83303 | H sapiens mRNA for granulocyte chemotactic protein | ? |
| 5243 | >10 | U89946 | Human brain secretory protein HSec10p (HSEC10) mRNA complete cds | other |
| 32789 | >10 | W02779 | ESTs Moderately similar to kinesin-T3 [O melanogaster] | other |
| 42354 | >10 | W19345 | ESTs | other |
| 42390 | >10 | W40150 | Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds | other |
| 33006 | >10 | W45236 | ESTs Weakly similar to ZK1058.5 [C.elegans] | TM |
| 33020 | >10 | W46891 | ESTs Weakly similar to polypeptide N-acetylglucosaminyltransferase [H sapiens] | other |
| 33109 | >10 | W59961 | Human mRNA for KIAA0359 gene complete cds | other |
| 24197 | >10 | W67277 | ESTs | other |
| 24215 | >10 | W69425 | ESTs | other |
| 33301 | >10 | W73883 | ESTs | other |
| 33343 | >10 | W79834 | ESTs Weakly similar to myosin [M musculus] | other |
| 33377 | >10 | W81219 | ESTs Weakly similar to F4986.7 [C.elegans] | other |
| 42622 | >10 | W86423 | ESTs | TM |
| 33556 | >10 | W90705 | Murine leukemia virus (Bmi-1) oncogene homolog | other |
| 33616 | >10 | W93726 | Protease inhibitor 5 (maspin) | other |
| 33666 | >10 | W95876 | ESTs | TM |
| 5510 | >10 | X05360 | Cell division cycle 2 G1 to S and G2 to M | ? |
| 5556 | >10 | X07676 | Wenches-type MMTV integration site 2 human homolog | SS |
| 5603 | >10 | X14253 | Teratocarcinoma-derived growth factor 1 | TM |
| 5619 | >10 | X14650 | HISTONE H2A X | SS |
| 5623 | >10 | X14975 | T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR | ? |
| 5692 | >10 | X17644 | G1 to S phase transition 1 | other |
| 5789 | >10 | X54925 | Matrix metalloproteinase 1 (interstitial collagenase) | other |
| 5799 | >10 | X55330 | Asparaginylglucosaminidase | SS |
| 5802 | >10 | X55544 | CYCLOC-AMP-DEPENDENT TRANSCRIPTION FACTOR AIF-1 | ? |
| 5857 | >10 | X58377 | Human mRNA for adipogenesis inhibitory factor | other |
| 5960 | >10 | X63575 | ATPase C+++ transporting plasma membrane 2 (NOXIE; redensin of symbol) | TM |
| 5963 | >10 | X63629 | Cadherin 3 (P-cadherin) | SS TM |
| 5986 | >10 | X64810 | Proprotein convertase subtilisin/kexin type 1 | ? |
| 6041 | >10 | X67155 | MITOTIC KINESIN-LIKE PROTEIN-1 | other |
| 6095 | >10 | X69962 | Fragile X mental retardation 1 | other |

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| | | | | |
|-------|--------------|--------------|---|--------|
| 6106 | >10 | X70683 | SRY (sex determining region Y)-box 4 | TM |
| 6155 | >10 | X74331 | DNA premase polypeptide 2A (SNA2) | other |
| 6167 | >10 | X74907 | Ribonuclease L (2'5' oligoadenylate synthetase-dependent) inhibitor | other |
| 6188 | >10 | X76029 | NEUROMEDIN U-25 PRECURSOR | TM |
| 6315 | >10 | X81889 | H sapiens mRNA for p0071 protein | other |
| 6382 | >10 | X85133 | H sapiens RBQ-1 mRNA | other |
| 6384 | >10 | X85137 | Human kinesin-like spindle protein HKSP (HKSP) | other |
| 6438 | >10 | X89398 | URACIL-DNA GLYCOSYLASE 1 PRECURSOR | ? |
| 6449 | >10 | X89985 | H sapiens mRNA for NIK apoptotic inducer protein | TM |
| 6478 | >10 | X91648 | H sapiens mRNA for put alpha extended 3'untranslated region | SS, TM |
| 6479 | >10 | X91653 | EST - X91653 | ? |
| 6494 | >10 | X92689 | H sapiens mRNA for UOP-GalNAc:polypeptide N-ethylglucosaminyl transferase | TM |
| 6713 | >10 | Y08564 | EST - Y08564 | ? |
| 6790 | >10 | Y12394 | Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds | other |
| 24915 | >10 | YEL003w | EST - YEL003w | ? |
| 42773 | >10 | YEL019cMM521 | EST - YEL019cMM521 | ? |
| 24545 | >10 | Z39462 | ESTs | other |
| 33713 | >10 | Z39427 | ESTs | other |
| 33791 | >10 | Z40883 | ESTs | other |
| 42766 | >10 | Z99394 | ESTs Moderately similar to H1 ALU SUBFAMILY SP WARNING ENTRY H1 [H sapiens] | other |
| 21558 | >10 | R33112 | Human AF-6 mRNA complete cds | other |
| 26718 | >10 | AA282576 | ESTs | ? |
| 40113 | 9 995090946 | H78003 | ESTs | ? |
| 10801 | 9 9879448276 | AA069285 | ESTs Weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R15E11.3 [C.elegans] | other |
| 37491 | 9 9513600842 | AA455239 | ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN OPY-127 [Caenorhabditis elegans] | other |
| 23900 | 9 9272347693 | T89789 | ESTs | other |
| 254 | 9 9198395324 | O14657 | Human mRNA for KIAA0101 gene complete cds | other |
| 6685 | 9 8970827914 | Z29331 | Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC9) | other |
| 29605 | 9 8650766398 | H97819 | ESTs | SS, |
| 26482 | 9 8765189024 | AA262491 | ESTs | other |
| 23123 | 9 8699502035 | T25306 | EST | ? |
| 20525 | 9 8160399123 | AA278392 | ESTs | other |
| 13110 | 9 7643356605 | AA435840 | Homo sapiens mRNA for high mobility group protein HMGB2 | other |
| 34863 | 9 7087597628 | AA299704 | EST | other |
| 39432 | 9 7034550083 | D51691 | Phosphoenolpyruvate carboxykinase formyltransferase phosphoenolpyruvate synthetase phosphoenolpyruvate synthetase | ? |
| 31312 | 9 6513325388 | N66845 | ESTs Weakly similar to H1 ALU CLASS B WARNING ENTRY H1 [H sapiens] | ? |
| 21112 | 9 6358446349 | R01179 | ESTs | ? |
| 31573 | 9 6254820695 | N71294 | ESTs | other |
| 17903 | 9 6221229759 | AA160259 | EST | ? |
| 20747 | 9 6094813734 | N66842 | ESTs | other |
| 4676 | 9 589223908 | U55206 | Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA complete cds | TM |
| 34363 | 9 5627081023 | AA251587 | Homo sapiens mRNA for KIAA0530 protein partial cds | other |
| 39094 | 9 540706898 | AA620036 | ESTs | other |
| 3886 | 9 5372000133 | U15126 | Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds | ? |
| 3886 | 9 502550629 | D12164 | ESTs | TM |
| 7674 | 9 4458059039 | AA203742 | ESTs | other |
| 4192 | 9 4329744134 | U10350 | Human DP prostanoid receptor (PTGDR) mRNA partial cds | TM |
| 4507 | 9 422674945 | U47050 | Human putative calcium influx channel (htrp3) mRNA complete cds | TM |

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| | | | | |
|-------|---------------|---------------|--|-------|
| 35005 | 9 412026255 | AA402227 | ESTs Moderately similar to N-tropomodulin [R. norvegicus] | other |
| 4970 | 9 3649551013 | U70862 | Human nuclear factor H2 (NFH2) mRNA complete cds | ? |
| 19929 | 9 3432151573 | H58813 | EST | ? |
| 14837 | 9 2878584141 | T40145 | ESTs | TM |
| 17330 | 9 2822146075 | AA099585 | ESTs | other |
| 40541 | 9 2532830505 | N30160 | ESTs | other |
| 29496 | 9 2487643833 | H85434 | EST | ? |
| 29943 | 9 1970747402 | N24786 | ESTs Moderately similar to HSA SUBFAMILY J WARNING ENTRY !!! [H. sapiens] | TM |
| 17997 | 9 1629691314 | AA189533 | EST | other |
| 21320 | 9 1243463318 | R11873 | ESTs | other |
| 13883 | 9 1178795537 | AA478917 | ESTs Weakly similar to No definition line found [C. elegans] | other |
| 30539 | 9 0886897778 | N49072 | ESTs | other |
| 32778 | 9 0877919549 | V02063 | EST | ? |
| 26380 | 9 0009559378 | AJ257012 | EST | ? |
| 15889 | 9 0059893607 | X95632 | Human Abi interactor 2 (Abi-2) mRNA complete cds | other |
| 40812 | 9 0012874244 | N63419 | ESTs | other |
| 903 | 9 9640387308 | D90070 | ATL-derived PMA-responsive (APR) peptide | other |
| 22674 | 9 9515777733 | R87160 | ESTs | TM |
| 40807 | 9 9510132281 | N82995 | TRANSCRIPTION INITIATION FACTOR IIF BETA SUBUNIT | other |
| 15244 | 9 9195644974 | V00904 | ESTs | TM |
| 32296 | 9 8658776567 | R67075 | Zinc finger protein X-linked | other |
| 18289 | 9 8575656789 | AJ209467 | ESTs | other |
| 19662 | 9 8507826284 | H47391 | ESTs | other |
| 41807 | 9 8339255117 | R87869 | CLEAVAGE SIGNAL-1 PROTEIN | other |
| 2548 | 9 8299864699 | M25897 | Platelet factor 4 | TM |
| 7730 | 9 8279341243 | AJ232121 | Human tyrosyl-tRNA synthetase mRNA complete cds | other |
| 34490 | 9 7844537272 | AA262354 | ESTs | other |
| 38658 | 9 7699313482 | AA595477 | ESTs | other |
| 7528 | 9 7851575554 | AA149543 | ESTs | other |
| 39939 | 9 7555031142 | H53454 | EST - RC_H53454 | other |
| 25111 | 9 7232692309 | AA020787 | ESTs | other |
| 21855 | 9 7181872779 | R38239 | EST | ? |
| 39683 | 9 665982852 | H04756 | ESTs Highly similar to NADH:UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Bos taurus] | other |
| 1042 | 9 652112324 | HG2510-HT2606 | EST - HG2510-HT2606 | ? |
| 32330 | 9 8361115426 | R77776 | ESTs | other |
| 25362 | 9 8239456487 | AA059007 | ESTs | other |
| 27074 | 9 8900813076 | AA401475 | ESTs Weakly similar to C32B1.3 [C. elegans] | SS |
| 3955 | 9 52090909183 | U18259 | MHC class II transactivator | other |
| 4959 | 9 52646627 | U70322 | Human transporter (TRN) mRNA complete cds | other |
| 2315 | 9 5259185808 | M14123 | EST - M14123_opt1 | ? |
| 37263 | 9 4890314632 | AA469357 | ESTs | other |
| 39624 | 9 471316877 | F10836 | ESTs | ? |
| 23213 | 9 4568952087 | T40891 | ESTs | ? |
| 2798 | 9 455506435 | M54995 | Connective tissue activation peptide II | TM |
| 41154 | 9 4413380141 | R07499 | ESTs | ? |
| 32479 | 9 4093689549 | T16782 | WEE1-LIKE PROTEIN KINASE | other |
| 41251 | 9 3587565415 | R28279 | Human clone 23548 mRNA sequence | other |
| 19081 | 9 3543603183 | H06701 | ESTs Weakly similar to RHOMBOTIN-1 [H. sapiens] | other |
| 21098 | 9 3105927559 | R00545 | ESTs | other |
| 14723 | 9 3061679053 | D58804 | ESTs | other |
| 39154 | 9 2994822341 | AA447666 | Human CENP-F kinesin core protein mRNA complete cds | other |

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| | | | | |
|-------|--------------|----------|---|-------|
| 8068 | 8 2835506361 | AA313387 | ESTs Highly similar to HYPOTHETICAL B4.7 KD PROTEIN ZK1059.1 IN CHROMOSOME II (Chromomolax elegans) | other |
| 7485 | 8 281873348 | AA129547 | ESTs | other |
| 16501 | 8 2517965834 | AA026969 | ESTs | other |
| 34527 | 8 2419163754 | AA279091 | ESTs | other |
| 6700 | 8 1940675902 | Y07667 | H sapiens mRNA for Pim isolate 1 | other |
| 2852 | 8 1928816537 | M58460 | Human 75-kD autoantigen (PM-Scl) mRNA complete cds | other |
| 11188 | 8 1862492498 | AA172372 | ESTs | TM |
| 42283 | 8 1853111064 | T95333 | ESTs Weakly similar to coded for by C elegans cDNA yA110g6.3 (C elegans) | TM |
| 5443 | 8 1763317544 | X02530 | Interferon (gamma)-induced cell line protein 10 from | SS |
| 49197 | 8 1534810594 | N70607 | ESTs | TM |
| 23371 | 8 1495496098 | T59505 | EST - RC_T59505 | ? |
| 26272 | 8 1339974519 | AA252981 | ESTs Weakly similar to K07C11.10 gene product (C elegans) | other |
| 17306 | 8 1332403762 | AA086201 | ESTs | other |
| 18497 | 8 1192325373 | AA233795 | ESTs | other |
| 235 | 8 0644363901 | D13644 | Human mRNA for KIAA0019 gene complete cds | other |
| 24525 | 8 0660187097 | Z38347 | ESTs | TM |
| 7828 | 8 0750028554 | AA240894 | EST - AA240894 | TM |
| 32142 | 8 0739258775 | R38715 | Homo sapiens clone 24540 mRNA sequence | other |
| 39067 | 8 0657768803 | AA620405 | ESTs | other |
| 8235 | 8 0448957336 | X78416 | Casem alpha S1 | TM |
| 29517 | 8 0017588725 | H88251 | ESTs | other |
| 28570 | 7 9952455973 | C21104 | Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds | other |
| 39344 | 7 9162087762 | C21034 | ESTs Moderately similar to invasion factor aIF-2B gamma subunit (R. norvegicus) | other |
| 18951 | 7 9002189759 | H00580 | ESTs | other |
| 18953 | 7 8709160227 | H00915 | ESTs | other |
| 19376 | 7 8564099916 | AA228925 | ESTs | other |
| 19830 | 7 841878447 | H56911 | ESTs | other |
| 36023 | 7 840835026 | AA415081 | ESTs | other |
| 13347 | 7 8344414518 | AA449238 | ESTs | other |
| 36814 | 7 8284561351 | AA431486 | ESTs | other |
| 2182 | 7 8254072032 | L48211 | Homo Sapiens angiotensin II receptor gene complete cds | ? |
| 33016 | 7 8000574068 | W65577 | H sapiens mRNA for ESM-1 protein | other |
| 17215 | 7 7941854038 | AA083044 | ESTs | other |
| 34894 | 7 7669738105 | AA311981 | EST | ? |
| 40614 | 7 7590901222 | N99257 | ESTs | other |
| 36295 | 7 6834749899 | AA424334 | ESTs | other |
| 19564 | 7 6744302786 | H88833 | ESTs | TM |
| 16914 | 7 6686405306 | AA050665 | ESTs | SS |
| 35967 | 7 6378079107 | AA412694 | Human splicing factor SRp55-2 (SRp55) mRNA complete cds | other |
| 21672 | 7 6364823402 | R30535 | ESTs | other |
| 19918 | 7 6303275831 | H69787 | ESTs | ? |
| 10511 | 7 6297144492 | AA024482 | ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 (Homo sapiens) | other |
| 17721 | 7 6057911016 | AA136590 | ESTs | ? |
| 42302 | 7 6031859697 | T06130 | EST | SS |
| 26134 | 7 6000619383 | AA243763 | ESTs | other |
| 18786 | 7 5621799008 | F09497 | ESTs | other |
| 34492 | 7 5015904094 | AA052439 | ATL-derived PMA-responsive (APR) peptide | other |
| 270 | 7 4512152125 | D14822 | EST - D14822 | other |
| 35975 | 7 4177746286 | AA412738 | ESTs | other |
| 29842 | 7 4055806371 | N21688 | ESTs | ? |

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| | | | | |
|-------|---------------|---------------|---|-------|
| 35369 | 7 3913043319 | AA399505 | ESTs | other |
| 19979 | 7 3868157195 | H88477 | ESTs | other |
| 5793 | 7 3955864025 | X54342 | CDC28 protein kinase 2 | other |
| 19978 | 7 387969715 | H87770 | EST - RC_H87770 | other |
| 1290 | 7 3691099318 | HG4126-HT4396 | EST - HG4126-HT4396 | ? |
| 31571 | 7 3676283454 | H71250 | ESTs | other |
| 23765 | 7 3541191734 | T30443 | ESTs Weakly similar to KIAA0376 [H sapiens] | ? |
| 35123 | 7 3397933455 | AA380927 | EST | ? |
| 38252 | 7 3341119467 | AA489247 | ESTs | other |
| 38216 | 7 3242021037 | AA488861 | ESTs | other |
| 29418 | 7 2489407005 | H77915 | EST - RC_H77915 | ? |
| 4834 | 7 1982951054 | U63541 | Human mRNA expressed in HCHCC livers and MoT-4 proliferating cells partial sequence | other |
| 42504 | 7 1913036522 | V65903 | ESTs | other |
| 6111 | 7 158000198 | X71125 | H sapiens mRNA for glutamine cyclotransferase | TM |
| 41773 | 7 154479618 | T03024 | ESTs Weakly similar to ribosomal protein L7 [H sapiens] | other |
| 9951 | 7 1363626365 | H71513 | ESTs | other |
| 28109 | 7 0941958224 | AA485212 | ESTs | other |
| 968 | 7 0783044659 | HG2160-HT2230 | EST - HG2160-HT2230 | ? |
| 29848 | 7 0610668511 | N22107 | ESTs | other |
| 30628 | 7 0607950168 | N50744 | ESTs | other |
| 22567 | 7 0251726353 | R77771 | ESTs | TM |
| 9347 | 7 005323071 | H03666 | ESTs | TM |
| 11696 | 7 0026773299 | AA252894 | ESTs | other |
| 40564 | 7 0010095333 | N34870 | EST | ? |
| 193 | 6 9767029108 | D10623 | PROBABLE G PROTEIN-COUPLED RECEPTOR HM74 | TM |
| 18305 | 6 9740536051 | AA214348 | Collagen type IV alpha 4 | other |
| 6078 | 6 9699082397 | X69141 | FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE | other |
| 26741 | 6 902658703 | AA203198 | ESTs | other |
| 35069 | 6 8992865686 | AA356397 | EST | ? |
| 23564 | 6 8977135683 | T71042 | ESTs | other |
| 299 | 6 8824513029 | D16815 | Human sapiens orphan nuclear hormone receptor BD73 | other |
| 40583 | 6 8689903023 | N34855 | ESTs | other |
| 31428 | 6 8623762224 | N68594 | ESTs | other |
| 6169 | 6 86069598727 | X75091 | SET PROTEIN | other |
| 39524 | 6 8567355171 | F01905 | MALATE OXIDOREDUCTASE | other |
| 34578 | 6 8430698439 | AA200037 | ESTs | other |
| 39678 | 6 837527995 | AA599920 | Small inducible cytokine A5 (RANTES) | other |
| 23930 | 6 8251471804 | T9693C | ESTs | other |
| 9236 | 6 8181321394 | D89377 | Msh (Drosophila) homeo box homolog 2 | other |
| 19186 | 6 8067351968 | H11255 | ESTs Highly similar to ACTIN-LIKE PROTEIN (Bos taurus) | TM |
| 18185 | 6 7882148811 | AA194983 | Human sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds | other |
| 27028 | 6 757429124 | AA399630 | ESTs Weakly similar to KIAA0371 [H sapiens] | other |
| 41289 | 6 7519531681 | R37365 | EST | other |
| 34511 | 6 7364448798 | AA278298 | EST - RC_AA278298 | other |
| 1566 | 6 7156207716 | J05614 | EST - J05614 | ? |
| 25675 | 6 6862299748 | AA120757 | ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus] | other |
| 5814 | 6 6584342828 | X56088 | CYTCHROME P450 VII | SS |
| 13861 | 6 6236291907 | AA470145 | ESTs | other |
| 29794 | 6 6026313352 | N20598 | ESTs | other |
| 39333 | 6 5902382643 | C20910 | Cyclin B1 | other |
| 3770 | 6 5835303599 | U09099 | Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (NFkBp100) | other |

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| | | | | |
|-------|---------------|----------|---|-------|
| 31831 | 6 5829933764 | N89894 | ESTs | ? |
| 33063 | 6 5808125026 | V53000 | Homo sapiens clone 24431 mRNA sequence | other |
| 20326 | 6 5640084836 | N25583 | ESTs Weakly similar to PROBABLE E5 PROTEIN [human papillomavirus type 56] | ? |
| 34384 | 6 5536703492 | AA252537 | ESTs | other |
| 25599 | 6 5450481991 | AA114091 | Human (clone BBT) B1-cadherin mRNA complete cds | other |
| 39749 | 6 5369363254 | H14988 | ESTs | other |
| 42596 | 6 5200567072 | V85900 | ESTs | ? |
| 39606 | 6 5119482185 | F10243 | ESTs Weakly similar to H1 ALU CLASS B WARNING ENTRY III [H.sapiens] | ? |
| 14617 | 6 5105504748 | C14983 | ESTs | other |
| 27831 | 6 45873814 | AA456044 | ESTs | ? |
| 34896 | 6 4496517703 | AA312551 | EST | ? |
| 27360 | 6 4434356006 | AA425356 | ESTs | other |
| 20126 | 6 4329510424 | N22015 | ESTs | TM |
| 6663 | 6 4324309977 | Y00291 | RETINOIC ACID RECEPTOR BETA-2 | TM |
| 30692 | 6 4196636207 | N51563 | ESTs | other |
| 36472 | 6 4189542285 | AA428633 | EST | ? |
| 9578 | 6 3951788753 | H87652 | Homo sapiens bcaudal-0 (BICD) mRNA complete cds | other |
| 39670 | 6 3818496159 | H05626 | ESTs | other |
| 22897 | 6 3652792447 | R89216 | ESTs | other |
| 37308 | 6 3647804993 | AA451654 | EST | TM |
| 16101 | 6 3517262902 | AA002147 | EST | ? |
| 20629 | 6 34396854401 | N59798 | ESTs | other |
| 36100 | 6 3364146287 | AA417740 | ESTs | ? |
| 15466 | 6 3252590241 | V29097 | Homo sapiens clone 23711 unknown mRNA partial cds | other |
| 36667 | 6 3131273544 | AA432136 | ESTs | other |
| 30766 | 6 3115007924 | N52627 | EST - RC_N52627 | ? |
| 32882 | 6 2745311453 | V97663 | ESTs | TM |
| 18072 | 6 2675797205 | AA180448 | EST | ? |
| 18231 | 6 2652604583 | AA199747 | Human mRNA for KIAA0096 gene partial cds | other |
| 36282 | 6 2514165678 | AA488814 | EST | ? |
| 28125 | 6 250317021 | AA486073 | ESTs | other |
| 37464 | 6 2484456382 | AA454747 | ESTs | ? |
| 36618 | 6 1946328223 | AA431478 | ESTs | other |
| 5082 | 6 1931116815 | U78524 | Human Gii binding protein mRNA partial cds | other |
| 1441 | 6 1777207039 | J02963 | Integrin alpha 2b (platelet glycoprotein IIb of fibrilla complex antigen CD41b) | other |
| 42105 | 6 14875944 | T67710 | ESTs | ? |
| 6061 | 6 1394863141 | B68314 | Glutathione peroxidase 2 gastrointestinal | 55, |
| 32570 | 6 1156028796 | T30222 | ESTs Weakly similar to tetracycline transporter-like protein [M.musculus] | TM |
| 32504 | 6 1019612076 | T17063 | EST | ? |
| 23335 | 6 0977927504 | T56804 | EST | ? |
| 10667 | 6 0970991075 | AA088458 | ESTs Weakly similar to H1 ALU 5U87FAMILY J WARNING ENTRY III [H.sapiens] | other |
| 30883 | 6 0911993489 | N56923 | EST | ? |
| 14528 | 6 0859006453 | AA620295 | ESTs | TM |
| 29454 | 6 0685955036 | H81308 | EST | ? |
| 6798 | 6 0539173278 | Y13153 | Homo sapiens mRNA for kynurenine 3-monooxygenase | TM |
| 21248 | 6 0525426545 | R08871 | ESTs | ? |
| 21940 | 6 0499964138 | R44538 | ESTs | ? |
| 29066 | 6 0455247653 | F10927 | Homo sapiens clone 23636 mRNA sequence | other |
| 18774 | 6 0446826953 | F09099 | ESTs | ? |
| 36722 | 6 0172345991 | AA435512 | ESTs | 55, |
| 18062 | 6 0034342969 | AA179845 | ESTs Moderately similar to rab39bun-6 [M.musculus] | other |

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| | | | | |
|-------|--------------|---------------|---|-------|
| 22989 | 5 9992817406 | T16305 | ESTs | other |
| 41745 | 5 9905623898 | R95895 | ESTs | ? |
| 8787 | 5 9894677658 | AA504367 | X-LINKED HEL CASE II | other |
| 20550 | 5 984861795 | N55013 | ESTs | other |
| 26470 | 5 9417764101 | AA362179 | ESTs | other |
| 16574 | 5 9355497569 | AA031926 | EST | other |
| 693 | 5 9169537385 | D80007 | Human mRNA for KIAA0165 gene partial cds | other |
| 4003 | 5 914830973 | U25182 | Human arylsulfatase enzyme ADE-37-2 mRNA complete cds | TM |
| 1192 | 5 9086265407 | HG3546-HT3744 | EST - HG3546-HT3744 | ? |
| 22956 | 5 8954735623 | T10248 | ESTs | other |
| 36723 | 5 8916065409 | AA435524 | EST | ? |
| 2114 | 5 8844966595 | L40384 | EST - L40384 | other |
| 26872 | 5 866238789 | AA291137 | ESTs | other |
| 6602 | 5 8663983018 | X98266 | EST - X98266_cds2 | other |
| 42701 | 5 8504403433 | Z38612 | ESTs | other |
| 28573 | 5 84591116 | C21118 | ESTs | other |
| 18290 | 5 8185427595 | AA211901 | ESTs | other |
| 732 | 5 8043917941 | D83781 | Human mRNA for KIAA0197 gene partial cds | other |
| 8330 | 5 8014145611 | U91327 | EST - U91327 | ? |
| 33503 | 5 7990715189 | W88720 | EST | ? |
| 2563 | 5 7797505864 | M26167 | Human platelet factor 4 variant 1 (PF4var1) gene complete cds | ? |
| 34705 | 5 7556806254 | AA386907 | ESTs Weakly similar to putative p150 [H sapiens] | other |
| 42665 | 5 7554091043 | W93659 | ESTs | other |
| 38180 | 5 7539310793 | AA487495 | EST - RC_AA487495 | other |
| 4244 | 5 7478738809 | U33286 | Human chromosome segregation gene homolog CAS mRNA complete cds | other |
| 32822 | 5 7418957453 | W16634 | ESTs | TM |
| 3977 | 5 7245885557 | U18991 | Retinal pigment epithelium-specific protein (RSPD) | ? |
| 24673 | 5 7202989155 | Z39301 | ESTs | TM |
| 6928 | 5 7120261128 | Z46629 | SRV (sex-determining region Y)-box 9 (campomic dysplasia autosomal sex-reverse) | other |
| 36726 | 5 7020796258 | AA608733 | ESTs | ? |
| 39290 | 5 6882372058 | C14573 | Human mRNA for KIAA0029 gene partial cds | other |
| 11405 | 5 6818873796 | AA232231 | ESTs | other |
| 22838 | 5 6792008691 | R73567 | Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds | TM |
| 40747 | 5 6605393328 | H56872 | Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds | TM |
| 31596 | 5 6554024604 | N72094 | ESTs | other |
| 6329 | 5 6415652518 | X82279 | EST - X82279 | ? |
| 31578 | 5 6273323661 | N71361 | ESTs | other |
| 33207 | 5 6271818482 | W70051 | H.sapiens mRNA for M-phase phosphoprotein mp99 | other |
| 2545 | 5 6105860140 | M25753 | Cyclin B1 | other |
| 22640 | 5 5988402647 | R79156 | ESTs | other |
| 33892 | 5 5938214518 | W99127 | ESTs | other |
| 28843 | 5 5734698755 | D00292 | ESTs | other |
| 6180 | 5 5689050619 | X74794 | CDC21 HOMOLOG | other |
| 37887 | 5 561345667 | AA479666 | ESTs | other |
| 42615 | 5 5521786811 | W72116 | Homo sapiens clone Z3622 mRNA sequence | other |
| 4732 | 5 5130668527 | U58522 | Human huntingtin interacting protein (HIP2) mRNA complete cds | other |
| 3299 | 5 5098850678 | M59623 | Hydroxymethylglutamate synthase | ? |
| 28320 | 5 473408391 | AA589574 | ESTs | ? |
| 746 | 5 471200899 | D84454 | Human mRNA for UDP-galactose translocator complete cds | TM |
| 39373 | 5 4635049454 | C21517 | ESTs | other |
| 3117 | 5 4398413537 | M81182 | Pericardial membrane protein 1 (70kD Zellweger syndrome) | other |

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| | | | | |
|-------|---------------|---------------|--|-------|
| 21257 | 5 4343612441 | R09196 | ESTs Moderately similar to M-phase phosphoprotein 11 [H sapiens] | other |
| 31487 | 5 4318048059 | N89507 | ESTs | other |
| 28954 | 5 4137130511 | F03153 | ESTs | other |
| 38928 | 5 389762721 | AA609595 | ESTs | other |
| 29503 | 5 3722329622 | H23386 | EST | ? |
| 30925 | 5 3437433315 | H58295 | ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H sapiens] | ? |
| 10001 | 5 3344615669 | H07864 | ESTs | TM |
| 28209 | 5 3138951919 | AA491250 | ESTs | other |
| 9470 | 5 3118807984 | H46617 | EST - H46617 | other |
| 9435 | 5 3070056656 | H30201 | EST - H30201 | ? |
| 28552 | 5 2954432872 | C20914 | ESTs | other |
| 27411 | 5 2940164267 | AA426137 | ESTs | other |
| 30615 | 5 2924125264 | H50556 | ESTs | other |
| 28313 | 5 2057977167 | AA599309 | ESTs | TM |
| 39321 | 5 2649035384 | C20632 | ESTs | ? |
| 29934 | 5 2531047395 | N24194 | ESTs | other |
| 1094 | 5 2496703122 | HQ2646-IT2993 | EST - HQ2646-IT2993 | ? |
| 39578 | 5 2481126384 | F08925 | ESTs | TM |
| 11232 | 5 2468794424 | AA186804 | ESTs Weakly similar to unknown [S cerevisiae] | other |
| 2466 | 5 2426349328 | M21539 | Human small proline rich protein (sprt) mRNA clone 1292 | other |
| 28843 | 5 2387756661 | AA287450 | ESTs | ? |
| 40331 | 5 2353365567 | H87562 | ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 (Sapae ofnalsat) | other |
| 8035 | 5 205789365 | AA305116 | EST - AA305116 | other |
| 29793 | 5 1955428722 | N20593 | ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C elegans] | other |
| 34109 | 5 1481590107 | AA210722 | EST | ? |
| 26408 | 5 1432577257 | AA258177 | ESTs Weakly similar to ROGA2GAS [M musculus] | other |
| 19263 | 5 1427029807 | H15054 | ESTs | TM |
| 24596 | 5 1416089352 | Z38810 | ESTs | other |
| 28569 | 5 1365089753 | C21245 | H sapiens mRNA for apoptosis specific protein | other |
| 5684 | 5 1121531412 | X17098 | Pregnancy-specific beta-1 glycoprotein 6 | other |
| 30710 | 5 1079347344 | N51761 | EST | ? |
| 35705 | 5 0973514948 | AA406167 | EST | ? |
| 26360 | 5 0963127861 | AA254460 | ESTs | ? |
| 2351 | 5 0849612092 | M15796 | Proliferating cell nuclear antigen | ? |
| 30262 | 5 0836877534 | N35065 | Human sapiens clone 24738 mRNA sequence | other |
| 41792 | 5 0737512405 | T03866 | ESTs | ? |
| 36710 | 5 0703835864 | AA434111 | ESTs | other |
| 39090 | 5 0546065407 | AA220628 | ESTs | TM |
| 42185 | 5 0539926381 | T79951 | ESTs | ? |
| 18745 | 5 0460321557 | F09134 | ESTs | other |
| 35746 | 5 03968641990 | AA400063 | ESTs | other |
| 35356 | 5 03548209581 | AA399053 | EST | ? |
| 36769 | 5 0312706878 | AA435750 | EST | ? |
| 36900 | 5 0279911548 | AA436866 | H sapiens mRNA for M-phase phosphoprotein mpp9 | other |
| 27595 | 5 0244757301 | AA443328 | ESTs | TM |
| 16290 | 5 0056611904 | AA016145 | ESTs | ? |
| 27117 | 5 0016140599 | AA405098 | ESTs Weakly similar to MOESIN/ELZRIN/RADIXIN HOMOLOG (D melanogaster) | other |
| 4304 | 4 9951954397 | U30764 | Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit | other |
| 33458 | 4 9907402071 | V60835 | Human sapiens mRNA for KIAA0636 protein complete cds | other |
| 26593 | 4 9800000679 | AA282120 | EST | ? |
| 12669 | 4 9758133051 | AA417030 | Human sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds | other |

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| | | | | |
|-------|--------------|---------------|---|--------|
| 29701 | 4 9706526387 | H97970 | EST | ? |
| 20480 | 4 9557253636 | N52168 | ESTs | TM |
| 8720 | 4 9439110602 | AA481218 | EST - AA481218 | other |
| 34828 | 4 9431269475 | AA092436 | Homo sapiens semaphorin F homolog mRNA complete cds | SS, TM |
| 14965 | 4 941621032 | U15128 | Human beta-12-N-acetylglucosaminyltransferase II (NGAT2) gene complete cds | ? |
| 16115 | 4 9377553522 | AA004420 | ESTs | ? |
| 42500 | 4 9345507118 | W70074 | EST | other |
| 34761 | 4 9316037445 | AA287833 | ESTs | other |
| 11870 | 4 9281056201 | AA252587 | ESTs | TM |
| 23211 | 4 9255391854 | T40689 | ESTs | other |
| 40611 | 4 9160502275 | N39138 | Homo sapiens mRNA for KIAA0594 protein partial cds | other |
| 42611 | 4 9128605354 | W87006 | Homo sapiens putative RNA binding protein KOC (koc) mRNA complete cds | other |
| 35652 | 4 9045174605 | K03099 | ESTs | other |
| 17581 | 4 889674751 | AA129395 | EST | ? |
| 37239 | 4 8704375369 | AA449121 | ESTs | ? |
| 18712 | 4 8703618781 | F04677 | ESTs | other |
| 30709 | 4 8611171953 | H51752 | ESTs Weekly similar to synapse-associated protein snap25.1 (D.melanogaster) | other |
| 34179 | 4 8503612948 | AA227903 | ESTs Highly similar to GTP-BINDING PROTEIN LEPA (Pseudomonas fluorescens) | other |
| 21433 | 4 8256709586 | R22183 | EST | ? |
| 39731 | 4 8186142741 | H11760 | ESTs | other |
| 31295 | 4 8116614607 | N66653 | ESTs | other |
| 24647 | 4 8041630555 | Z39108 | EST | ? |
| 31292 | 4 8009871817 | N66615 | ESTs | other |
| 1285 | 4 7997542293 | HG4157-HT4427 | EST - HG4157-HT4427 | ? |
| 1106 | 4 7932425858 | HG2981-HT3127 | EST - HG2981-HT3127 | ? |
| 18212 | 4 7912262965 | AA196506 | ESTs | other |
| 34367 | 4 782207045 | AA251758 | Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds | other |
| 34802 | 4 7797760205 | AA291468 | ESTs | TM |
| 34762 | 4 7775301546 | AA387634 | ESTs | other |
| 11595 | 4 7699612848 | AA342619 | ESTs | other |
| 8295 | 4 7639859111 | AA405082 | ESTs | ? |
| 17622 | 4 756635576 | AA131584 | ESTs Weekly similar to SOF1 PROTEIN [Saccharomyces cerevisiae] | other |
| 38781 | 4 7572463523 | AA406335 | ESTs | other |
| 34754 | 4 7483674972 | AA287642 | Human mRNA for KIAA0078 gene complete cds | other |
| 23237 | 4 7444854356 | T47291 | EST | ? |
| 37667 | 4 7280445357 | AA460318 | ESTs Highly similar to 60S RIBOSOMAL PROTEIN L26 [Rattus norvegicus] | other |
| 11568 | 4 7267189975 | AA336786 | ESTs | other |
| 38622 | 4 7190695733 | AA598967 | ESTs | ? |
| 5137 | 4 7067556474 | U75296 | Dihydroxyacetone S-acyltransferase (E2 component of pyruvate dehydrogenase complex) | other |
| 25038 | 4 7002244728 | AA010065 | CDK28 protein kinase 2 | other |
| 19288 | 4 7000147312 | H16567 | ESTs | other |
| 32503 | 4 6979486292 | T17045 | Collagen type I alpha2 | other |
| 3278 | 4 6953739258 | M94055 | SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT | TM |
| 9595 | 4 6942061018 | L39161 | Integral transmembrane protein 1 | TM |
| 35400 | 4 690130698 | AA389691 | Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds | other |
| 35246 | 4 6862691303 | AA368367 | EST Weekly similar to HSP60 protein [M.musculus] | ? |
| 36387 | 4 6822499271 | AA426270 | ESTs | other |
| 21509 | 4 6730072542 | R27314 | ESTs | other |
| 31381 | 4 6729672124 | N67889 | ESTs | other |
| 26723 | 4 6727894925 | AA382781 | ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP28 [Saccharomyces cerevisiae] | other |

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| | | | | |
|-------|---------------|----------------------|---|--------|
| 36326 | 4 6703621086 | AA425151 | Human GAP SH3 binding protein mRNA, complete cds | other |
| 17409 | 4 6688418067 | AA113136 | EST - RC_AA113136 | other |
| 4906 | 4 6552339935 | U67156 | Human mitogen-activated kinase kinase kinase 5 (MAP3K5) mRNA, complete cds | other |
| 30594 | 4 6496230328 | N49967 | ESTs | other |
| 38286 | 4 646539735 | AA489647 | ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Nycotian glauca] | ? |
| 13073 | 4 6426509459 | AA433950 | ESTs | other |
| 40435 | 4 6240181066 | N21614 | Homo sapiens basic leucine zipper transcription factor MafK (MAFK) mRNA, complete cds | other |
| 14474 | 4 62206094379 | AA609427 | ESTs Moderately similar to III ALU 5 SUBFAMILY 5C WARNING ENTRY III [H.sapiens] | ? |
| 30213 | 4 6153309007 | AA486847 | ESTs Weakly similar to putative p150 [H.sapiens] | ? |
| 5312 | 4 6066441190 | U90716 | Human cell surface protein HCAR1 mRNA, complete cds | 55, TM |
| 24225 | 4 6041550059 | W70326 | ESTs | ? |
| 35588 | 4 58698982366 | AA401750 | EST | ? |
| 29739 | 4 58653190051 | H99626 | EST | ? |
| 7203 | 4 5792992577 | AA053096 | EST - AA053096 | other |
| 2157 | 4 5772055669 | L41939 | Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA, complete cds | 55, TM |
| 32990 | 4 5661024279 | R11510 | ESTs | ? |
| 8065 | 4 5648114738 | AA314779 | ESTs Weakly similar to LITHO6 TATHINE 1 BETA PRECURSOR [H.sapiens] | 55, |
| 224 | 4 5622018989 | D13633 | Human mRNA for KIAA0009 gene, complete cds | other |
| 34006 | 4 5609980241 | AA188761 | CNA polymerase gamma | other |
| 33056 | 4 5587384389 | V95477 | ESTs | other |
| 34065 | 4 5537335124 | AA195517 | ESTs Weakly similar to III ALU 5 SUBFAMILY J WARNING ENTRY III [H.sapiens] | TM |
| 6028 | 4 5357622097 | X66503 | Adenylosuccinate synthetase | other |
| 4186 | 4 5032930671 | U29463 | Cytochrome B561 | ? |
| 40262 | 4 5024727522 | H93562 | ESTs | TM |
| 22667 | 4 5010672549 | R86209 | ESTs | TM |
| 41069 | 4 4977510482 | N93959 | H.sapiens mRNA for hFAT protein | SS, |
| 8264 | 4 47931100575 | AA401334 | ESTs | other |
| 27668 | 4 472017287 | AA443187 | ESTs | other |
| 35882 | 4 4717897552 | AA412047 | ESTs | ? |
| 34479 | 4 465519191 | AA262090 | Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds | TM |
| 15921 | 4 45485164536 | Y12065 | Homo sapiens mRNA for nucleolar protein hNop56 | ? |
| 11279 | 4 4360036671 | AA195399 | ESTs | other |
| 39222 | 4 4367650796 | AA621348 | ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae] | other |
| 34428 | 4 4364736766 | AA256526 | ESTs | other |
| 8771 | 4 432067373 | AA491188 | ESTs | other |
| 22193 | 4 4189610024 | R50891 | Homo sapiens mRNA from chromosome 5q21-22 clone A3-A | other |
| 7898 | 4 4006170674 | AA263032 | ESTs | other |
| 19902 | 4 3806145805 | H66736 | ESTs | other |
| 6276 | 4 3868096209 | D62374 | ESTs | other |
| 10716 | 4 3784529068 | AA053319 | ESTs | TM |
| 13193 | 4 3751913512 | AA442763 | ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus] | other |
| 5690 | 4 3723059417 | X17620 | NUCLEOSIDE DIPHOSPHATE KINASE A | other |
| 35102 | 4 37147138 | AA371509 | EST - RC_AA371509 | TM |
| 17983 | 4 3612985467 | AA168225 | ESTs | other |
| 24962 | 4 3497206925 | AFFX-HUMTFRFRM115_07 | AFFX-HUMTFRFRM115_07_5 | ? |
| 31680 | 4 3416539069 | N74438 | ESTs | other |
| 27168 | 4 330306894 | AA410253 | ESTs | other |
| 28731 | 4 3231846659 | D20981 | EST | ? |
| 28348 | 4 3212284906 | AA606752 | ESTs | other |

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| | | | | |
|-------|--------------|----------------------|--|-------|
| 16336 | 4.3019961467 | AA018587 | ESTs Weakly similar to H1ALU SUBFAMILY SP WARNING ENTRY !!! [H sapiens] | ? |
| 33036 | 4.2915644973 | W46580 | ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H sapiens] | other |
| 30180 | 4.2897721925 | N33144 | ESTs | other |
| 35591 | 4.2895541242 | AA401758 | ESTs Weakly similar to H1ALU SUBFAMILY SQ WARNING ENTRY !!! [H sapiens] | SS |
| 25340 | 4.2721717135 | AA054554 | EST | ? |
| 28106 | 4.2659103748 | AA485084 | ESTs | other |
| 38690 | 4.2649194307 | AA6000121 | ESTs | other |
| 20203 | 4.2626499431 | N26555 | ESTs Moderately similar to H1ALU SUBFAMILY SQ WARNING ENTRY !!! [H sapiens] | other |
| 10251 | 4.2608760694 | R76185 | ESTs Weakly similar to CD116.7 [C elegans] | SS |
| 12684 | 4.2604192389 | AA417558 | ESTs | SS |
| 31636 | 4.2509460427 | N73650 | Natural resistance-associated macrophage protein 2 | TM |
| 20769 | 4.2479765348 | N67277 | ESTs | other |
| 1572 | 4.2363201063 | K01884 | EST - K01884 | ? |
| 10623 | 4.2293222072 | AA116036 | ESTs | other |
| 34360 | 4.2283782362 | AA252414 | ESTs | other |
| 10132 | 4.2222816115 | R35733 | EST - R35733 | other |
| 18629 | 4.2161752119 | AA036811 | ESTs | other |
| 25146 | 4.1996963794 | AA026356 | ESTs | ? |
| 28730 | 4.1965943090 | D20559 | ESTs Moderately similar to H1ALU SUBFAMILY SQ WARNING ENTRY !!! [H sapiens] | other |
| 10200 | 4.1874912391 | R64521 | ESTs | other |
| 38695 | 4.1545794663 | AA600176 | ESTs | other |
| 31365 | 4.150549679 | N67550 | ESTs | other |
| 42379 | 4.1496120658 | D27899 | ESTs | other |
| 26550 | 4.1428733354 | AA479139 | Acid phosphatase 1 soluble | other |
| 2620 | 4.1386555707 | M29474 | Human recombinational activating protein (RAG-1) gene complete cds | ? |
| 8927 | 4.1340593744 | AF008442 | Homo sapiens RNA polymerase I subunit HRP439 mRNA complete cds | other |
| 13379 | 4.1268549188 | AA449741 | ESTs Weakly similar to Af-9 PROTEIN [H sapiens] | other |
| 5134 | 4.1218251806 | U75293 | Human clone 23948 mRNA sequence | other |
| 2820 | 4.12119848 | M29581 | Zinc finger protein 8 (clone HF 18) | other |
| 38005 | 4.1180483666 | AA479969 | ESTs | other |
| 36575 | 4.1127196584 | AA431085 | EST | ? |
| 15296 | 4.1121037207 | AA213620 | ESTs Weakly similar to putative p100 [H sapiens] | ? |
| 26531 | 4.1111459313 | H88953 | EST - HC_H88953 | TM |
| 143 | 4.1095800506 | AFFX-HUMTFRRM11507_5 | AFFX-HUMTFRRM11507_5 | ? |
| 10970 | 4.0967613396 | AA129380 | ESTs | other |
| 25636 | 4.0952826397 | AA152305 | Interferon (gamma)-induced cell line protein 10 from | SS |
| 19735 | 4.0937927853 | H53038 | EST | ? |
| 40711 | 4.0909700431 | N83564 | ESTs | other |
| 4149 | 4.0901471427 | U20386 | RAG (recombination activating gene) cohort 1 | TM |
| 5767 | 4.0862784557 | X53793 | MULTIFUNCTIONAL PROTEIN ADE2 | other |
| 5503 | 4.0861036825 | X05232 | Stemelysin | SS |
| 20310 | 4.0841711656 | N34893 | ESTs Highly similar to HYPOTHETICAL 47.8 KB PROTEIN B0280.9 IN CHROMOSOME III [Caenorhabditis elegans] | other |
| 456 | 4.0595824566 | D38145 | Prostaglandin I2 (prostaglandin) synthase | SS |
| 7814 | 4.0559685676 | AA248406 | ESTs | other |
| 40230 | 4.0447282719 | H90161 | ESTs | SS |
| 33651 | 4.0392048004 | W95409 | ESTs | other |
| 16777 | 4.0231657929 | AA348968 | EST | ? |
| 19110 | 4.0064906222 | H08718 | ESTs | other |
| 34442 | 4.0077010365 | AA258093 | HKR-T1 | other |
| 5099 | 4.0049924233 | U73247 | Human clone 23399 mRNA sequence | TM |

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| | | | | |
|-------|--------------|------------------------|--|--------|
| 8209 | 3 5990473163 | AA364220 | ESTs | other |
| 24408 | 3 9976586074 | W90146 | ESTs | other |
| 26596 | 3 9974919187 | AA275943 | ESTs | other |
| 16485 | 3 9811264008 | AA026269 | Spleen focus forming virus (SFFV) proviral integration oncogene sp1 | other |
| 22969 | 3 9804901745 | W42451 | ESTs | TM |
| 27006 | 3 9799758093 | AA359695 | ESTs Weakly similar to E04F5.2 gene product [C.elegans] | other |
| 23909 | 3 9526765967 | N21043 | EST | ? |
| 9596 | 3 9440163451 | H91564 | ESTs | TM |
| 29024 | 3 9377933938 | F09315 | Homo sapiens mRNA for KIAA0583 protein partial cds | other |
| 21694 | 3 9336365504 | R35317 | Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds | other |
| 13297 | 3 9299991104 | AA463321 | ESTs | other |
| 37865 | 3 9143752829 | AA776623 | ESTs Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe] | other |
| 36201 | 3 9129828172 | AA421164 | ESTs | ? |
| 8961 | 3 8961160269 | AFX-HUMTFRRM11507_3 | AFX-HUMTFRRM11507_3 | ? |
| 17444 | 3 8927133917 | AA115933 | ESTs | other |
| 25969 | 3 8919834527 | AA157267 | ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN Z6586.3 IN CHROMOSOME III [Caenorhabditis elegans] | TM |
| 24962 | 3 89042252 | Z41415 | ESTs Highly similar to BONE MORPHOGENETIC PROTEIN-1 PRECURSOR [Mus musculus] | other |
| 26685 | 3 889363206 | AA281950 | ESTs | ? |
| 42300 | 3 8850203066 | T95850 | ESTs | ? |
| 6495 | 3 8830644863 | X52715 | Zinc finger protein 74 (Cox52) | other |
| 38604 | 3 8828045942 | AA598803 | ESTs | TM |
| 36358 | 3 8826713718 | AA425756 | ESTs | other |
| 30560 | 3 873275445 | N45284 | MYB PROTO-ONCOGENE PROTEIN | other |
| 14413 | 3 8724461658 | AA600150 | ESTs | other |
| 23823 | 3 8574824967 | T91805 | Homo sapiens mRNA for ST1C2 complete cds | other |
| 38198 | 3 853096938 | AA487021 | EST | ? |
| 2572 | 3 8519747554 | M27281 | Vascular endothelial growth factor | other |
| 40100 | 3 8464166867 | H75933 | Laminin receptor (2HS epitope) | other |
| 40258 | 3 8462892993 | H53340 | ESTs | TM |
| 20944 | 3 8461621525 | N74443 | ESTs | other |
| 20411 | 3 8459400966 | N49393 | Homo sapiens mRNA for KIAA0685 protein partial cds | other |
| 10345 | 3 8457174481 | AA001683 | ESTs | other |
| 31261 | 3 8451874374 | N66248 | EST | other |
| 8513 | 3 8378410994 | AA469990 | ESTs | other |
| 13877 | 3 8363409835 | AA476604 | ESTs | other |
| 40748 | 3 8253622321 | N56879 | EST | ? |
| 14509 | 3 8152852193 | AA609943 | ESTs | other |
| 10281 | 3 8065567331 | R80333 | ESTs | other |
| 25284 | 3 8044156642 | AA045074 | ESTs Weakly similar to 52-kD S5-A/Ro autoantigen [H. sapiens] | other |
| 6730 | 3 7900025129 | Y09305 | H. sapiens mRNA for protein kinase Dyrk4 partial | other |
| 16033 | 3 7884392402 | AFX-HUMISGF3AM57935_M8 | AFX-HUMISGF3AM57935_M8 | ? |
| 39242 | 3 7827164808 | AA521523 | ESTs | other |
| 27354 | 3 7794780435 | AA425221 | ESTs | ? |
| 4552 | 3 777263605 | U49188 | Human placenta (DIT83) mRNA complete cds | SS, TM |
| 18385 | 3 7756195108 | AA227219 | Homo sapiens CAGF9 mRNA partial cds | other |
| 16754 | 3 7677410053 | AA046057 | EST - RC_AA046057 | other |
| 12752 | 3 7671137403 | AA421250 | ESTs | other |
| 42463 | 3 7601033106 | W60180 | ESTs | other |

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| | | | | |
|-------|---------------|-----------|---|-------|
| 10614 | 3 7581669016 | AA037357 | ESTs | ? |
| 867 | 3 7459337069 | D87716 | Human mRNA for KIAA0007 gene partial cds | other |
| 7608 | 3 7336047135 | AA180967 | ESTs | other |
| 31796 | 3 732758742 | N80703 | ESTs | other |
| 35377 | 3 7273704603 | AA399453 | EST - RC_AA399453 | ? |
| 22828 | 3 7243928524 | R98192 | ESTs | other |
| 25240 | 3 7243190336 | AA009713 | ESTs | other |
| 11008 | 3 7197361366 | AA134289 | ESTs Weakly similar to ASH1 [D.melanogaster] | ? |
| 4341 | 3 7162349944 | U36545 | Human ARF-activated phosphatidylcholine-specific phospholipase D 1a (HPLD1) mRNA complete cds | other |
| 28833 | 3 7147818393 | D59787 | EST - RC_D59787 | ? |
| 3750 | 3 7121007154 | U9279 | Collagen type XIX alpha 1 | SS. |
| 17483 | 3 6943413512 | AA122147 | ESTs | TM |
| 16854 | 3 6915208471 | AA055552 | ESTs Weakly similar to KIAA0319 [H.sapiens] | TM |
| 3709 | 3 6891656771 | U07550 | Heat shock 10 KD protein 1 (chaperonin 10) | other |
| 1608 | 3 6652978422 | L00205 | KERATIN TYPE II CYTOSKELETAL 60 | ? |
| 24577 | 3 6617721053 | Z38727 | Homo sapiens mRNA for KIAA0555 protein complete cds | TM |
| 31032 | 3 6570916386 | N62506 | ESTs | other |
| 4941 | 3 65361195433 | U65545 | Human RNA binding protein E1v-3 mRNA complete cds | other |
| 37560 | 3 6523275307 | AA460225 | ESTs | other |
| 20418 | 3 6495357091 | H92209 | ESTs | other |
| 27995 | 3 6485167436 | AA470155 | Homo sapiens coatomer protein (COP) mRNA complete cds | ? |
| 7971 | 3 6434397185 | AA287423 | ESTs | other |
| 27606 | 3 64303453 | AA440793 | ESTs | other |
| 24577 | 3 6427250633 | Z39338 | ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus] | other |
| 11070 | 3 6405198277 | AA145521 | ESTs Weakly similar to putative p150 [H.sapiens] | TM |
| 9328 | 3 6356046599 | D95618 | Homo sapiens importin-alpha homolog (SRP1 gamma) mRNA complete cds | other |
| 36826 | 3 6346889802 | AA1435996 | ESTs | other |
| 17676 | 3 6300046756 | AA134276 | Human: HIV1 15' element modulatory factor mRNA sequence from chromosome 3 | other |
| 96209 | 3 6274684477 | AA421266 | ESTs Weakly similar to LIS-1 protein [H.sapiens] | other |
| 34120 | 3 6258090412 | AA211615 | EST | ? |
| 36152 | 3 6246442011 | AA486737 | H.sapiens mRNA for Sm protein F | TM |
| 36463 | 3 6154693266 | AA504491 | ESTs Weakly similar to contains similarity to C3HC4-class zinc finger [C.elegans] | TM |
| 20064 | 3 6163699978 | H96053 | ESTs | TM |
| 31256 | 3 5992620732 | N66152 | EST | ? |
| 9713 | 3 5985228843 | L44338 | Homo sapiens mRNA for KIAA0525 protein partial cds | other |
| 29622 | 3 5766506147 | D11837 | ESTs | ? |
| 38057 | 3 5736105703 | AA481549 | EST - RC_AA481549 | other |
| 28763 | 3 5688723791 | D45568 | EST | ? |
| 18996 | 3 5680705709 | AA069035 | EST - RC_AA069035 | TM |
| 28628 | 3 5604144617 | D11888 | ESTs Moderately similar to PROHIBITIN [H.sapiens] | ? |
| 25604 | 3 5442354572 | AA148885 | ESTs | ? |
| 2492 | 3 5423954239 | M22898 | Tumor protein p53 (L-Fraumeni syndrome) | ? |
| 14904 | 3 5411570737 | T83389 | ESTs Highly similar to GEFHYRIN [Rattus norvegicus] | other |
| 25265 | 3 5347588502 | AA043765 | H.sapiens RY-1 mRNA for putative nucleic acid binding protein | other |
| 19606 | 3 5327912417 | AA455437 | ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens] | other |
| 42307 | 3 5318436465 | T96595 | EST - RC_T96595 | TM |
| 1544 | 3 528202414 | J05069 | TRANSCOBALAMIN I PRECURSOR | SS. |
| 42339 | 3 5195061035 | WC2072 | ESTs Weakly similar to No definition line found [C.elegans] | other |
| 42311 | 3 51833719631 | T97257 | ESTs | other |
| 2023 | 3 5040275423 | L34600 | INITIATION FACTOR IF-2 MITOCHONDRIAL PRECURSOR | other |

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| | | | | |
|-------|---------------|----------|---|--------|
| 4540 | 3 4955306569 | U48607 | Human MAP kinase phosphatase (MKP-2) mRNA complete cds | other |
| 33707 | 3 4886534277 | Z33297 | Neuronal pentraxin II | other |
| 17220 | 3 4756763461 | AJ063070 | EST - RC_AA083070_s | SS |
| 24332 | 3 4725273606 | V65782 | ESTs | other |
| 35887 | 3 4668063718 | AA410067 | ESTs | other |
| 20158 | 3 4538150055 | N23638 | ESTs Weakly similar to coded for by C. elegans cDNA YK224.10 (C. elegans) | other |
| 8338 | 3 4465832071 | AA117152 | Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds | other |
| 387 | 3 4421427234 | D28589 | EST - D28589 | other |
| 12319 | 3 4366209717 | AA398109 | ESTs | SS, TM |
| 38276 | 3 4313139432 | AA489711 | ESTs | TM |
| 15643 | 3 4312194246 | V58247 | ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus] | other |
| 11218 | 3 4232023843 | AA180488 | ESTs | TM |
| 16539 | 3 417886379 | AJ029328 | Human mRNA for KIAA0073 gene partial cds | ? |
| 29203 | 3 4162847487 | H28581 | ESTs | other |
| 13838 | 3 4162403464 | AA465342 | ESTs | other |
| 25585 | 3 4160353003 | AA112389 | H4D105170) | SS |
| 34018 | 3 4145338583 | AA191488 | Human high-affinity copper uptake protein (HCTR1) mRNA complete cds | TM |
| 251 | 3 4030042851 | D14520 | Basic transcription element binding protein 2 | other |
| 3778 | 3 4004516201 | U09648 | Zinc finger protein 139 (clone pIZ-37) | other |
| 24355 | 3 3964397637 | Z38409 | ESTs | other |
| 16858 | 3 3925194041 | AJ055759 | Human mRNA for KIAA0128 gene partial cds | TM |
| 16127 | 3 3921645927 | AJ004669 | ESTs | other |
| 36683 | 3 38411316491 | AA432266 | ESTs | other |
| 26149 | 3 3809497785 | AA250824 | ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens] | other |
| 4011 | 3 3798093471 | U20536 | Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds | other |
| 41001 | 3 3794250205 | N78844 | ESTs | other |
| 5660 | 3 3789336731 | X16396 | NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE | SS |
| 19204 | 3 3778332343 | H11629 | ESTs | other |
| 42323 | 3 3768515979 | T98152 | Fertilin 2 | SS |
| 26928 | 3 3725378868 | AA342560 | ESTs | SS |
| 20497 | 3 3692859812 | N52665 | ESTs | other |
| 19226 | 3 36674249 | H12455 | ESTs | other |
| 36287 | 3 3639661638 | AA424046 | ESTs | other |
| 32257 | 3 3559796018 | R54726 | DNA-REPAIR PROTEIN XRCC1 | other |
| 17365 | 3 3522214732 | AA101551 | ESTs | other |
| 15296 | 3 3491193196 | V16684 | ESTs Moderately similar to Similar to S cerevisiae hypothetical protein L3111 [H. sapiens] | other |
| 17675 | 3 3465870272 | AA134004 | ESTs | TM |
| 40332 | 3 34564669589 | H97565 | Homo sapiens mRNA from chromosome 5q21-22 clone A3-A | other |
| 7219 | 3 3385664843 | AA056319 | Homo sapiens protein phosphatase 2A (55c-epsilon) (PP2A) mRNA complete cds | other |
| 10006 | 3 3323227922 | N81193 | Homo sapiens mRNA for KIAA0628 protein complete cds | ? |
| 33965 | 3 3276877441 | AA181580 | Homo sapiens importin beta subunit mRNA complete cds | other |
| 9570 | 3 3263855302 | H85169 | Homo sapiens sodium/ATP-independent cotransporter (SLC5A3) gene complete cds | other |
| 37551 | 3 3155406577 | AA456679 | ESTs | other |
| 886 | 3 3111782759 | D88613 | Human mRNA for hGCMs complete cds | other |
| 23650 | 3 3069426629 | T86293 | ESTs | other |
| 18367 | 3 3007433533 | AA224180 | ESTs Moderately similar to ovarian-specific protein [R. norvegicus] | ? |
| 42494 | 3 2988070546 | V69385 | H. sapiens HsAA gene (Clone T33) | other |
| 14310 | 3 2753564661 | AA598412 | ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PMR16-PC11 INTERGENIC REGION [Saccharomyces cerevisiae] | SS, TM |

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| | | | | |
|-------|--------------|----------------------|---|-------|
| 19233 | 3.274415299 | H12634 | ESTs | other |
| 42283 | 3.2731066284 | T94343 | Homo sapiens MKI2 protein spliced isoform 2 mRNA complete cds | other |
| 12809 | 3.271352097 | AA424406 | ESTs | other |
| 36285 | 3.2696023617 | AA424469 | ESTs | other |
| 21555 | 3.2663266446 | RC33073 | EST | ? |
| 13767 | 3.2665695616 | AA463234 | ESTs | TM |
| 4738 | 3.2661591937 | U56766 | Human FK protein mRNA complete cds | other |
| 7258 | 3.263106966 | AA075427 | ESTs | other |
| 17041 | 3.2629042076 | AA070364 | EST - RC_AA070364 | ? |
| 15504 | 3.2616745245 | V28362 | ESTs | other |
| 23793 | 3.2611829896 | T30971 | EST - RC_T30971 | other |
| 18214 | 3.2572346955 | AA196635 | ESTs | TM |
| 7401 | 3.2571694123 | AA094800 | Human translation initiation factor eIF3 p65 subunit mRNA complete cds | other |
| 18912 | 3.2553500001 | F10913 | Homo sapiens clone Z3917 unknown mRNA partial cds | other |
| 36317 | 3.2509495347 | AA425089 | Human mRNA for KIAA0334 gene complete cds | ? |
| 9410 | 3.2507279851 | H20443 | H sapiens mRNA for TRE5 | other |
| 2146 | 3.2464307896 | L41390 | EST - L41390 | ? |
| 18683 | 3.240814336 | F04256 | ESTs Highly similar to INORGANIC PYROPHOSPHATASE (Bos taurus) | ? |
| 33891 | 3.2392191408 | AFFX_HUMTFRAM11507_M | AFFX_HUMTFRAM11507_M | ? |
| 14435 | 3.2372161315 | AA608730 | ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA (Giardia intestinalis) | other |
| 9584 | 3.2363829855 | H88128 | ESTs Highly similar to GTP-BINDING PROTEIN LEPA (Pseudomonas fluorescens) | other |
| 22061 | 3.2340098572 | R49216 | ESTs | TM |
| 35796 | 3.233287805 | AA410223 | EST - RC_AA410223 | ? |
| 37403 | 3.2281852043 | AA453613 | ESTs | other |
| 15796 | 3.2280359888 | X16889 | ALPHA-GALACTOSIDASE A PRECURSOR | SS |
| 15840 | 3.2257932439 | X70844 | PTB-ASSOCIATED SPLICING FACTOR | other |
| 7518 | 3.2252170427 | AA147144 | EST - AA147144 | other |
| 32335 | 3.2228388982 | R78248 | ESTs | other |
| 3256 | 3.2160538038 | M92429 | 130 KD LEUCINE RICH PROTEIN | other |
| 4400 | 3.2173986081 | U41387 | Human Gu protein mRNA partial cds | other |
| 7681 | 3.2074414299 | AA205983 | Homo sapiens mRNA for DRIM protein | other |
| 15676 | 3.2041299443 | V68649 | ESTs | TM |
| 39590 | 3.2038952621 | F09281 | ESTs | other |
| 28883 | 3.1980022253 | AA291921 | ESTs Weakly similar to putative p150 (H sapiens) | ? |
| 9808 | 3.1920380384 | M80627 | Transcription factor 12 (HTF4 helix-loop-helix transcription factor 4) | other |
| 27755 | 3.1900699454 | AA453444 | ESTs | other |
| 29983 | 3.1862280623 | N28011 | ESTs | ? |
| 21350 | 3.1876195756 | R15846 | ESTs | other |
| 11981 | 3.1870625747 | AA280028 | ESTs | other |
| 23930 | 3.1817500097 | T96690 | ESTs Weakly similar to H1 ALU SUBFAMILY J | other |
| 30399 | 3.1792054412 | N52226 | EST | ? |
| 22286 | 3.1781990049 | R59312 | ESTs | other |
| 13494 | 3.1673900969 | AA453431 | ESTs | TM |
| 12908 | 3.1530532441 | AA427579 | ESTs | other |
| 22319 | 3.1469419301 | R00667 | ESTs | TM |
| 31309 | 3.1466750623 | N66818 | ESTs | TM |
| 31192 | 3.1456779823 | N64406 | ESTs | other |
| 11288 | 3.144853134 | AA196512 | ESTs | TM |
| 170 | 3.1430726349 | D00596 | Thymidylate synthase | ? |
| 5307 | 3.1347905028 | U90549 | Human non-histone chromosomal protein (NHC) mRNA complete cds | other |

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| | | | | |
|-------|--------------|----------|---|-------|
| 26105 | 3 1311103325 | AA243133 | Homo sapiens serine/threonine kinase (BIAK) mRNA complete cds | other |
| 11659 | 3 1281786108 | AA251909 | Homo sapiens MAD3-like protein kinase mRNA complete cds | other |
| 19177 | 3 124405655 | H10984 | ESTs | TM |
| 8389 | 3 1241545824 | AA425230 | ESTs | TM |
| 34087 | 3 1215553797 | AA205125 | Protein serine/threonine kinase sk2 | other |
| 25001 | 3 120627466 | AA004718 | ESTs Weakly similar to BAF31 protein (H sapiens) | other |
| 14149 | 3 1198500308 | AA489665 | ESTs | other |
| 10167 | 3 1191906393 | R55076 | ESTs | other |
| 17390 | 3 1071055868 | AA102566 | ESTs | other |
| 42397 | 3 1044606828 | W42923 | ESTs | other |
| 14935 | 3 1042015743 | T94828 | ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN (H sapiens) | other |
| 41673 | 3 1030349819 | R76618 | ESTs Weakly similar to GTP-binding protein rab10 (R. norvegicus) | other |
| 2750 | 3 1026223619 | M35999 | Integrin beta 3 (platelet glycoprotein IIb antigen CD61) | ? |
| 3190 | 3 1026223619 | M85808 | PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR | ? |
| 17406 | 3 0999394188 | AA112979 | Homo sapiens mRNA for VRK1 complete cds | other |
| 598 | 3 0912414004 | D59253 | Homo sapiens mRNA for low molecular mass ubiquitinone-binding protein complete cds | other |
| 29246 | 3 0822365759 | H69021 | ESTs | other |
| 14130 | 3 0744457534 | AA489041 | ESTs | other |
| 14134 | 3 069660341 | AA489080 | ESTs Highly similar to phosphorylation regulatory protein MP-10 (H sapiens) | other |
| 42421 | 3 0684159011 | W65421 | ESTs Weakly similar to T23G11.7 (C elegans) | other |
| 15723 | 3 0660740209 | W79050 | ESTs Highly similar to ribosome-binding protein p34 (R. norvegicus) | other |
| 11140 | 3 0650815198 | AA158132 | ESTs Highly similar to YSA1 PROTEIN (Saccharomyces cerevisiae) | other |
| 28531 | 3 0648787087 | C20678 | ESTs | other |
| 2021 | 3 0628707497 | L34409 | Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment | ? |
| 14522 | 3 0582601683 | AA810100 | ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G2 IE11.05C (Schizosaccharomyces pombe) | SS, |
| 29853 | 3 0545821815 | N22162 | ESTs | other |
| 15962 | 3 0521475703 | Z21410 | ESTs | other |
| 6541 | 3 0500806038 | X35632 | Human Abi interactor 2 (Abi-2) mRNA complete cds | other |
| 13229 | 3 0465366537 | AA443811 | ESTs | other |
| 27315 | 3 046632812 | AA424038 | ESTs | other |
| 13621 | 3 0302306368 | AA456821 | ESTs Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (Mus musculus) | other |
| 35929 | 3 0289182409 | AA112429 | ESTs | other |
| 17925 | 3 0253428426 | AA164209 | Homo sapiens RRM RNA binding protein Gyr-tp (GRY-RBP) mRNA complete cds | other |
| 5053 | 3 0249536782 | U76992 | Human Tel-SF1 mRNA complete cds | other |
| 15060 | 3 0213263848 | U54999 | Human LGN protein mRNA complete cds | other |
| 17757 | 3 0205801351 | AA147224 | EST | ? |
| 19050 | 3 0192379314 | H05509 | ESTs | other |
| 26530 | 3 0176623278 | AA273650 | ESTs | other |
| 16806 | 3 0158779932 | AA053258 | Homo sapiens mRNA for KIAA054B protein partial cds | TM |
| 29068 | 3 0145440394 | F13700 | Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds | other |
| 22960 | 3 0141662421 | T10272 | ESTs | other |
| 33585 | 3 0121672451 | W93000 | ESTs | other |
| 220 | 3 0105180714 | D13627 | Human mRNA for KIAA0002 gene complete cds | TM |
| 4298 | 3 0024671054 | U30448 | Human Ca2+-dependent activator protein for secretion mRNA complete cds | TM |
| 7445 | 2 9995643641 | AA104023 | ESTs | ? |
| 49903 | 2 9990347058 | N68670 | ESTs | ? |
| 18055 | 2 9973380648 | AA179387 | ESTs | other |
| 7282 | 2 9962792595 | AA063339 | ESTs | other |

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| | | | | |
|-------|--------------|---------------|--|-------|
| 9348 | 2 9949017671 | H03686 | ESTs | TM |
| 806 | 2 9877476515 | D87009 | Human (lambda) DNA for immunoglobulin light chain | ? |
| 38447 | 2 9876031644 | AA504255 | Human protein kinase ATR mRNA complete cds | other |
| 41464 | 2 9870604581 | R46837 | ESTs | ? |
| 9662 | 2 9869352306 | L19161 | TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT | other |
| 16976 | 2 9801154057 | AA063625 | EST | ? |
| 37426 | 2 9756406909 | AA454016 | ESTs | other |
| 2503 | 2 9725858208 | M27878 | Zinc finger protein 84 (HPF2) | other |
| 15174 | 2 9695024378 | U82987 | Human Bcl-2 binding component 3 (bbc3) mRNA partial cds | other |
| 33620 | 2 9657446567 | W93943 | ESTs | other |
| 6784 | 2 965506112 | Y11581 | Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds | ? |
| 41077 | 2 9642389716 | H95028 | ESTs | TM |
| 1932 | 2 9609585095 | L24804 | Human (p23) mRNA complete cds | other |
| 39556 | 2 9550964022 | F03738 | ESTs | other |
| 16108 | 2 9574232912 | AA002258 | ESTs | SS, |
| 32156 | 2 9574232912 | R40381 | ESTs | ? |
| 13617 | 2 9552305838 | AA456646 | ESTs | other |
| 11989 | 2 955203991 | AA281251 | ESTs Weekly similar to trithorax protein bnd1 [D.melanogaster] | other |
| 6056 | 2 947854132 | X68194 | Pantaprysin [human keratinocyte line HaCat] mRNA 7156 nt | TM |
| 15446 | 2 9445456286 | V027374 | Homo sapiens 10kD protein (BC10) mRNA complete cds | other |
| 38086 | 2 9445277634 | AA482557 | EST | ? |
| 13878 | 2 9444133384 | AA478604 | ESTs | other |
| 6209 | 2 9422435032 | X76770 | H sapiens PAP mRNA | other |
| 388 | 2 9357591919 | D28791 | Phosphatidylinositol glycan class A (paroxysmal nocturnal hemoglobinuria) | ? |
| 1351 | 2 9298145582 | HG4755-HT5203 | EST - HG4755-HT5203 | ? |
| 42624 | 2 9288145582 | W87804 | ESTs | other |
| 34895 | 2 9242794509 | AA311972 | ESTs | other |
| 20157 | 2 9214162976 | N23393 | ESTs | other |
| 28248 | 2 9188102156 | H62918 | ESTs | ? |
| 4893 | 2 9178533564 | U96615 | Human SWI/SNF complex 155 kDa subunit (BAF155) mRNA complete cds | other |
| 10104 | 2 9150324864 | R23855 | ESTs | TM |
| 15039 | 2 9147218324 | U46116 | Protein tyrosine phosphatase receptor type gamma polypeptide | ? |
| 1605 | 2 9141775797 | L00058 | V-myc avian myelocytomatous viral oncogene homolog | ? |
| 4536 | 2 907560336 | U48705 | Receptor protein-tyrosine kinase EDDR1 | ? |
| 10173 | 2 905710589 | R56678 | ESTs Weekly similar to ccd division control protein CDC21 [H.sapiens] | ? |
| 26555 | 2 9056210172 | AA279071 | ESTs Weekly similar to T06A11.2 [C.elegans] | other |
| 4401 | 2 9047655582 | U41515 | Human deleted in split hand/split foot 1 (DSS1) mRNA complete cds | other |
| 21009 | 2 8995011918 | N50401 | ESTs | TM |
| 3602 | 2 894817322 | U01317 | HEMOGLOBIN EPSILON CHAIN | ? |
| 4833 | 2 8919254016 | U63455 | Sulfonamide receptor (hypensulinemia) | ? |
| 36200 | 2 8912301426 | AA421154 | ESTs | ? |
| 26645 | 2 8898309441 | AA281076 | ESTs | other |
| 35299 | 2 8887661574 | AA398022 | Transcription factor 6-like 1 (mitochondrial transcription factor 1-like) | other |
| 9804 | 2 8880347344 | M74558 | Human SLL mRNA complete cds | other |
| 5216 | 2 8877077515 | U83410 | Human CUL-2 (cul-2) mRNA complete cds | other |
| 12313 | 2 8847621603 | AA397916 | ESTs | other |
| 5928 | 2 8836000438 | X62048 | WEE1-LIKE PROTEIN KINASE | ? |
| 39586 | 2 8818258313 | F09155 | ESTs | TM |
| 34758 | 2 8775214637 | AA287680 | EST | ? |
| 18199 | 2 8753649024 | AA195318 | ESTs | other |

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|-------|--------------|---------------|--|--------|
| 19067 | 2.8720574609 | H61476 | ESTs | ? |
| 6081 | 2.8679372906 | X69398 | CD47 antigen (Rb-related antigen integrin-associated signal transducer) | SS, TM |
| 5254 | 2.862087235 | U86782 | Human 2S protease-inhibitor-associated par1 homolog (POH1) mRNA complete cds | other |
| 13579 | 2.8570620494 | AA455967 | Human neuronal PAS2 (NPAS2) mRNA complete cds | ? |
| 1117 | 2.8568053461 | HG3075-HT3236 | EST - HG3075-HT3236 | ? |
| 20533 | 2.8564070641 | N54407 | ESTs | TM |
| 38495 | 2.8562453397 | AA505118 | Human nucleoporin 98 (NUP98) mRNA complete cds | other |
| 33729 | 2.8548155651 | Z39654 | EST | ? |
| 2028 | 2.8532776139 | L35035 | RIBOSE 5-PHOSPHATE ISOMERASE | other |
| 27374 | 2.8520674335 | AA425816 | ESTs Weakly similar to Y53C12A.3 [C.elegans] | other |
| 19404 | 2.8518630748 | HQ0568 | ESTs | other |
| 26108 | 2.8504706329 | AA243189 | ESTs | SS |
| 4189 | 2.8439972255 | U30930 | UDP glycosyltransferase 8 (UDP-galactose ceramide glucosyltransferase) | TM |
| 16708 | 2.8427388072 | AA043944 | ESTs | other |
| 357 | 2.8350474214 | D26156 | Human mRNA for transcriptional activator hSNF2b complete cds | other |
| 26045 | 2.8315740098 | AA336276 | ESTs | other |
| 17796 | 2.8312342777 | AA150435 | ESTs | other |
| 8059 | 2.8289722809 | AA310597 | ESTs Weakly similar to T04A8.11 [C.elegans] | other |
| 42014 | 2.8279999684 | N89220 | ESTs | other |
| 27189 | 2.8263163852 | AA410287 | H.sapiens mRNA for basic transcription factor 2.34 kD isoform | other |
| 21358 | 2.8262413945 | R16079 | ESTs | other |
| 3572 | 2.8261469131 | S87789 | Protein phosphatase 2C alpha [human teratocarcinoma mRNA 2346 nt] | other |
| 11877 | 2.8259099942 | AA262727 | ESTs | other |
| 1663 | 2.8234017508 | L05424 | CD44 antigen (cell adhesion molecule) | ? |
| 24645 | 2.8131264428 | Z39106 | ESTs | other |
| 35830 | 2.8126257031 | AA411448 | ESTs | TM |
| 4433 | 2.8114422177 | U43279 | EST - U43279 | ? |
| 20151 | 2.8109454503 | N22895 | Homo sapiens clone 1400 unknown protein mRNA partial cds | other |
| 36848 | 2.8084431065 | AA599267 | EST - RC_AA599267 | other |
| 7777 | 2.8071817829 | AA236820 | ESTs | other |
| 32845 | 2.80563194 | V91566 | EST | ? |
| 28258 | 2.8043934182 | AA505133 | ESTs | other |
| 6853 | 2.798263202 | Z22951 | TRANSCRIPTION FACTOR P65 | ? |
| 35844 | 2.7913872906 | AA412488 | ESTs | ? |
| 30648 | 2.7866523676 | N50971 | ESTs | ? |
| 18965 | 2.7857482775 | H01411 | ESTs | TM |
| 8616 | 2.785444221 | AA460077 | ESTs | other |
| 14845 | 2.7838257917 | T99606 | ESTs Weakly similar to F35G2.2 [C.elegans] | other |
| 8375 | 2.7805657722 | AA422160 | H.sapiens NAP (nucleosome assembly protein) mRNA complete cds | other |
| 34920 | 2.7782111121 | AA342084 | EST - RC_AA342084 | other |
| 326 | 2.7780978435 | D21262 | Human mRNA for KIAA0035 gene partial cds | other |
| 27057 | 2.7781215063 | AA400998 | ESTs | SS |
| 36292 | 2.7746002184 | AA424513 | EST - RC_AA424513 | other |
| 6480 | 2.7735431318 | X91788 | H.sapiens mRNA for Icn protein | other |
| 15424 | 2.7731675808 | W27054 | APOLIPROTEIN A1 REGULATORY PROTEIN-1 | other |
| 11602 | 2.7730818255 | AA243007 | ESTs | ? |
| 18175 | 2.77056686 | AA194730 | ESTs | ? |
| 25202 | 2.7698505996 | AA034527 | EST | ? |
| 1681 | 2.7697545972 | L07493 | Replication protein A (E.coli RecA homolog RAD51 homolog) | other |
| 14566 | 2.767884858 | AA521122 | ESTs | other |
| 25614 | 2.7633374335 | AA115769 | ESTs | other |

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|-------|---------------|---------------|---|-------|
| 14182 | 2 7606048934 | AA490885 | ESTs | other |
| 31599 | 2 7591187658 | N72196 | EST | other |
| 18253 | 2 74717646081 | AA206370 | ESTs | other |
| 6193 | 2 7442487702 | X76992 | Regulatory factor (trans-acting) 3 | other |
| 22911 | 2 7433449859 | T03865 | ESTs | other |
| 35549 | 2 743346595 | AA401274 | Homo sapiens RRM RNA binding protein Gty-rip (GRY- RBP) mRNA, complete cds | other |
| 35955 | 2 7389431758 | AA12528 | ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus Release (IS nonrepetitive) | other |
| 17642 | 2 7377607284 | AA132983 | ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [H sapiens] | other |
| 6131 | 2 7371784571 | X72841 | Human retinoblastoma-binding protein (RbAp48) mRNA complete cds | other |
| 41429 | 2 7347564467 | R44994 | ESTs | other |
| 17052 | 2 7323944161 | AA070815 | EST - RC_AA070815 | other |
| 34243 | 2 7294147034 | AA235050 | ESTs | ? |
| 22937 | 2 7284347248 | T10065 | Homo sapiens TLS-associated protein TASR-2 mRNA complete cds | other |
| 5183 | 2 7243199196 | U82130 | Human tumor susceptibility protein (TSG101) mRNA complete cds | other |
| 30837 | 2 7231409239 | N54416 | ESTs | other |
| 16243 | 2 72280026265 | AA012902 | ESTs | TM |
| 19954 | 2 7215193495 | H80100 | ESTs | other |
| 6444 | 2 720441384 | X69750 | H sapiens mRNA for TGIF protein | other |
| 5616 | 2 7192259481 | X61072 | Human mRNA for T cell receptor clone IGRA17 | SS. |
| 6240 | 2 7158544194 | X78627 | H sapiens mRNA for transin | ? |
| 42116 | 2 71441176166 | T69924 | EST - RC_T69924 | other |
| 7701 | 2 7107230466 | AA215333 | ESTs | TM |
| 17568 | 2 7096978968 | AA128905 | ESTs | TM |
| 42534 | 2 7085014274 | V73169 | Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds | SS TM |
| 29813 | 2 708372123 | N21111 | ESTs | other |
| 38898 | 2 7067394943 | AA609458 | ESTs | other |
| 10316 | 2 7055836457 | R88880 | ESTs Moderately similar to zinc finger protein [M musculus] | other |
| 14769 | 2 7040821965 | S54641 | H27-16 | other |
| 32961 | 2 7012196407 | V08366 | Human mRNA for KIAA0005 gene complete cds | other |
| 35273 | 2 6975345483 | AA388507 | ESTs | other |
| 19180 | 2 6960696303 | R60100 | ESTs | ? |
| 32963 | 2 6955482902 | T27897 | Human mRNA for KIAA0036 gene complete cds | other |
| 34502 | 2 6948574449 | AA262768 | ESTs | TM |
| 13223 | 2 6912995353 | AA443720 | ESTs | other |
| 8484 | 2 6906515739 | AA443460 | ESTs | other |
| 7776 | 2 6900717526 | AA236771 | ESTs | other |
| 10400 | 2 6898956951 | AA007234 | ESTs | other |
| 1130 | 2 6897527819 | HG3132-HT3308 | EST - HG3132-HT3308 | ? |
| 2379 | 2 6874247447 | M16037 | Human homeo box c1 protein mRNA complete cds | TM |
| 18906 | 2 6861450774 | F10868 | Human SH3 domain-containing protein SH3P18 mRNA complete cds | ? |
| 34796 | 2 6853510115 | AA291259 | ESTs | TM |
| 41955 | 2 6821406177 | T33311 | Neuronal pentraxin II | other |
| 2009 | 2 6791061739 | L33881 | Protein kinase C iota | ? |
| 33688 | 2 6775081286 | Z38501 | ESTs Weakly similar to PROBABLE E5 PROTEIN [human papillomavirus type 50] | other |
| 1305 | 2 6771402007 | HG8844-HT884 | EST - HG8844-HT884 | ? |
| 34758 | 2 6756083868 | Z40075 | ESTs | other |
| 7620 | 2 6742348913 | AA192484 | ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PHOSPHATASE SUBUNIT 2 [S cerevisiae] | other |
| 30733 | 2 6739544496 | N52078 | Homo sapiens mRNA for KIAA0637 protein complete cds | other |
| 21256 | 2 6723253005 | R05195 | Homo sapiens mRNA for KIAA0664 protein partial cds | other |
| 40528 | 2 668020450 | N26325 | ESTs Highly similar to 47 KD PROTEIN [Pseudomonas] | other |

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|-------|---------------|----------|---|--------|
| | | | chlorophylls] | |
| 25285 | 2.6685455408 | AA045063 | VITAMIN K DEPENDENT GAMMA-CARBOXYLASE | other |
| 9296 | 2.667949532 | D82775 | ESTs Weakly similar to unknown [S.cerevisiae] | SS |
| 12174 | 2.6669035328 | AA292128 | ESTs | other |
| 38357 | 2.6652770538 | AA491265 | EST | TM |
| 3154 | 2.6619536806 | M83712 | Cholinergic receptor nicotinic alpha polypeptide 5 | TM |
| 7383 | 2.655440738 | AA053834 | ESTs Weakly similar to HYPOTHETICAL 15.8 KD PROTEIN IN SMY2-RPS101 INTERGENIC REGION [S.cerevisiae] | other |
| 1923 | 2.6530772325 | L23808 | Matrix metalloproteinase 12 (macrophage elastase) | SS |
| 24906 | 2.6527348053 | Z41940 | ESTs | other |
| 34726 | 2.6495430564 | AA267278 | ESTs | SS |
| 30407 | 2.6495430564 | N45983 | ESTs | TM |
| 20408 | 2.6459091347 | N48787 | ESTs Moderately similar to 5th ALU SUBFAMILY SC WARNING ENTRY 111 [H.sapiens] | other |
| 7158 | 2.6455059455 | AA037206 | ESTs | TM |
| 26286 | 2.6445109706 | AA213351 | ESTs | ? |
| 19822 | 2.6431964212 | H56684 | ESTs | ? |
| 12379 | 2.6428192941 | AA399418 | Human sapient mRNA for JM23 protein complete coding sequence (clone IMAGE 34561 and IMAGE 45355 and LULU11013337 (R2PD Berlin)) | other |
| 22698 | 2.6396306055 | R18287 | ESTs | other |
| 24161 | 2.6394302284 | V95815 | ESTs | other |
| 9588 | 2.6370149706 | H81497 | ESTs | TM |
| 18104 | 2.6356787288 | AA188801 | ESTs | other |
| 24862 | 2.6357246889 | Z41563 | ESTs | other |
| 40036 | 2.6347874764 | H69485 | ESTs | other |
| 8865 | 2.6344845492 | AB020359 | Human mRNA for KIAA0361 gene KIAA0361 protein | other |
| 22148 | 2.6288326906 | R51831 | ESTs | other |
| 4627 | 2.627706831 | U51990 | Human hPrp18 mRNA complete cds | other |
| 8394 | 2.6275394634 | AA426156 | ESTs | TM |
| 20422 | 2.6272199716 | N46300 | ESTs | other |
| 41602 | 2.6268613624 | R67258 | ESTs Moderately similar to rhodopsin [M.musculus] | other |
| 612 | 2.6257836682 | D63480 | Human mRNA for KIAA0146 gene partial cds | TM |
| 4821 | 2.619521444 | U02801 | Human preprose M mRNA complete cds | SS, TM |
| 18807 | 2.617722928 | AA053296 | ESTs | other |
| 15286 | 2.6173997018 | V07562 | ESTs Moderately similar to rA8 [R.norvegicus] | other |
| 38023 | 2.6135617291 | AA481066 | ESTs | other |
| 23822 | 2.6120077647 | T91715 | ESTs Highly similar to HYPOTHETICAL 103.6 KD PROTEIN IN COX5B-PFK26 INTERGENIC REGION [Saccharomyces cerevisiae] | TM |
| 10951 | 2.6116018519 | AA126719 | ESTs | other |
| 6150 | 2.6113980879 | X74262 | RETINOBLASTOMA BINDING PROTEIN: P48 | other |
| 39336 | 2.6109987712 | C20945 | ESTs Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae] | other |
| 17793 | 2.6102158178 | AA152342 | ESTs Highly similar to modulator recognition factor 2 [H.sapiens] | other |
| 26891 | 2.6085107387 | AA293659 | ESTs | other |
| 2175 | 2.6074505576 | L42621 | Human sapiens Ly-9 mRNA complete cds | TM |
| 10642 | 2.6048724507 | AA040149 | Human Chromosome 15 BAC clone C1187SK-A-270A31 | other |
| 15026 | 2.6031453592 | U41816 | Human C-1 mRNA complete cds | other |
| 7699 | 2.6019047419 | AA215299 | Human sapiens chromosome 19 contig R20783 | other |
| 6543 | 2.6011828937 | X35654 | Human sapiens mRNA for SCP-1 complete cds | other |
| 20636 | 2.5993664878 | N52122 | ESTs | other |
| 11308 | 2.5992311375 | AA207114 | ESTs | other |
| 4286 | 2.5963628505 | U24704 | Human antisecretory factor-1 mRNA complete cds | other |
| 38615 | 2.59639596726 | AA598928 | EST - RC_AA598928 | other |
| 11819 | 2.59615021909 | AA258189 | ESTs | other |

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| | | | | |
|-------|---------------|----------|--|-------|
| 37433 | 2 5957446266 | AA454103 | ESTs | other |
| 28270 | 2 5839657529 | AA521186 | ESTs | TM |
| 5587 | 2 5832338399 | X13482 | U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A | other |
| 19841 | 2 5830132063 | H59517 | ESTs Highly similar to UBQUITIN-CONJUGATING ENZYME E-2-17 KD [Eosiphia melanogaster] | other |
| 10655 | 2 5925442731 | AA040882 | ESTs | ? |
| 14053 | 2 5895324577 | AA485147 | ESTs Highly similar to HYPOTHETICAL 83 6 KD PROTEIN R65D3.2 IN CHROMOSOME III [Caenorhabditis elegans] | other |
| 31574 | 2 5883094453 | N71303 | EST | ? |
| 7614 | 2 5870099315 | AA187579 | ESTs Weakly similar to Yel007c-op [S cerevisiae] | other |
| 37971 | 2 5847445397 | AA479195 | EST | ? |
| 7090 | 2 5845365105 | AA009913 | Homo sapiens diphthamide biosynthesis protein-2 (DIP2) mRNA complete cds | other |
| 17852 | 2 5841100415 | AA156300 | ESTs | other |
| 24219 | 2 5823376094 | V63960 | ESTs | other |
| 19070 | 2 5813645258 | H05870 | Human clone 23860 mRNA sequence | other |
| 17719 | 2 5803696155 | AA130569 | EST | ? |
| 38669 | 2 579196791 | AA599594 | Human mRNA for KIAA0133 gene complete cds | TM |
| 20982 | 2 57830557078 | N79585 | ESTs | TM |
| 9156 | 2 5731038907 | D31446 | Homo sapiens breakpoint cluster region protein 1 (BCR1) mRNA complete cds | other |
| 11302 | 2 5731137778 | AA227261 | ESTs | other |
| 8613 | 2 57233119462 | AA459555 | Homo sapiens mRNA for KIAA0648 protein partial cds | TM |
| 13868 | 2 5716907844 | AA476319 | ESTs | SS |
| 10303 | 2 5712815907 | R85178 | Ataxia telangiectasia mutated (includes complementation groups A C and D) | ? |
| 22299 | 2 567916035 | R59601 | EST | ? |
| 18257 | 2 5673459606 | AA200591 | EST - RC_AA200591 | other |
| 20555 | 2 5654242588 | N55188 | ESTs | other |
| 39552 | 2 5645918108 | F03605 | PUTATIVE 60S RIBOSOMAL PROTEIN | other |
| 27530 | 2 5631130948 | AA435999 | ESTs | other |
| 1785 | 2 5608471478 | L13434 | Human chromosome 3p21.1 gene sequence complete cds | ? |
| 14746 | 2 5603154968 | D60354 | Human mRNA for KIAA0007 gene partial cds | other |
| 2993 | 2 5587815672 | M64929 | Protein phosphatase 2 (formerly 2A) regulatory subunit B (PP2B) alpha isoform | other |
| 19191 | 2 5545260975 | H11297 | ESTs | other |
| 12986 | 2 5507999853 | AA430032 | ESTs Moderately similar to PTTG gene product [R norvegicus] | ? |
| 15452 | 2 5438533684 | V027451 | Human Cdc5-related protein (PCDC5RP) mRNA complete cds | other |
| 18003 | 2 5485671712 | AA171692 | ESTs | other |
| 24198 | 2 5481854497 | V67524 | Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence | TM |
| 42953 | 2 5447526827 | V80703 | ESTs | other |
| 26446 | 2 544106171 | AA258796 | EST Weakly similar to putative p150 [H sapiens] | ? |
| 30438 | 2 5388548574 | N47204 | ESTs Weakly similar to CSOF4.12 [C.elegans] | other |
| 36365 | 2 5362912735 | AA425893 | ESTs Weakly similar to proboscis CBP3 protein homolog [C.elegans] | other |
| 28135 | 2 535688968 | AA243165 | ESTs | other |
| 41885 | 2 5349932888 | T23449 | ESTs Moderately similar to ZNF127-Xp [H sapiens] | SS |
| 15487 | 2 5343495968 | V027660 | ESTs | other |
| 27748 | 2 5320767519 | AA453159 | Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds | other |
| 32315 | 2 5320797955 | R69840 | ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Hydrophis coarctatus] | ? |
| 25310 | 2 5274407579 | AA046745 | ESTs | other |
| 42720 | 2 5222453766 | Z39436 | ESTs | other |
| 12939 | 2 5200945911 | AA428204 | ESTs | other |
| 30746 | 2 5198420998 | N52743 | ESTs | other |
| 2222 | 2 5193624578 | L76703 | Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA complete cds | ? |
| 11609 | 2 5191785645 | AA243303 | ESTs | TM |

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| | | | | |
|-------|--------------|----------|--|--------|
| 9656 | 2 5185814336 | L16951 | Deoxythymidylate kinase | other |
| 12210 | 2 5172046681 | AA293774 | ESTs Weakly similar to PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE MITOCHONDRIAL [C elegans] | other |
| 3563 | 2 5169916533 | S83364 | EST - S83364 | other |
| 42407 | 2 5128230047 | W44768 | Homo sapiens nephrocytin (NHP1) mRNA partial cds | ? |
| 32826 | 2 5128052161 | VQ20391 | Human mRNA for known-related protein partial cds | other |
| 9652 | 2 5119977118 | L37747 | LAMIN B1 | ? |
| 27862 | 2 5094571267 | AA459608 | ESTs | TM |
| 33691 | 2 508287494 | Z38630 | EST | other |
| 17288 | 2 5088624644 | AA085178 | ESTs | SS |
| 9888 | 2 5076170902 | N35449 | ESTs highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/AP4/CWP-1 INTERGENIC REGION [Saccharomyces cerevisiae] | other |
| 5932 | 2 5073880985 | X82153 | Minichromosome maintenance deficient (S. cerevisiae) 3 | other |
| 15885 | 2 5053862932 | X95073 | H. sapiens mRNA for transin associated protein X | other |
| 17952 | 2 5049193223 | AA165677 | ESTs Weakly similar to F16A11.1 [C elegans] | other |
| 12197 | 2 5042458391 | AA293205 | ESTs | other |
| 6210 | 2 5042034458 | X76942 | Homo sapiens golgin-245 mRNA complete cds | other |
| 34047 | 2 5041917773 | AA194105 | ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H. sapiens] | other |
| 16929 | 2 5034461307 | AA658952 | ESTs | other |
| 26634 | 2 5029079692 | AA287138 | ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] | other |
| 5157 | 2 5017270258 | U80C34 | Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds | other |
| 38434 | 2 5005890672 | AA497013 | ESTs | ? |
| 33269 | 2 5000262771 | W72967 | ESTs | other |
| 26961 | 2 4990009911 | AA388284 | ESTs | other |
| 7590 | 2 4948786183 | AA173505 | ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PWO2-POL2 INTERGENIC REGION [S. cerevisiae] | other |
| 14960 | 2 4895232664 | U05237 | Human fetal Aiz-50-reactive clone 1 (FAC1) mRNA complete cds | other |
| 13586 | 2 4866732502 | AA455999 | ESTs Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa] | other |
| 35901 | 2 4847673158 | AA412151 | ESTs | other |
| 38185 | 2 4828740426 | AA487506 | Homo sapiens mRNA for KIAA0688 protein complete cds | other |
| 34678 | 2 4824371274 | AA284744 | Annonin XI (56kD autoantigen) | other |
| 1424 | 2 4811153231 | J02645 | Eukaryotic translation initiation factor 2A | other |
| 16778 | 2 4800522256 | AA047008 | ESTs | other |
| 21878 | 2 4789052023 | R43286 | EST - RC_R43286 | ? |
| 17779 | 2 4695725489 | AA149641 | ESTs | other |
| 24559 | 2 4682754649 | Z38588 | ESTs | other |
| 7781 | 2 457947166 | AA242904 | Homo sapiens proline-rich Gie protein 1 (PRGP1) mRNA complete cds | ? |
| 7474 | 2 4577129013 | AA126592 | ESTs Weakly similar to No deletion site found [C. elegans] | other |
| 34290 | 2 4575279697 | AA236866 | ESTs | other |
| 5316 | 2 4573813483 | U91905 | Human clone 23574 mRNA sequence | TM |
| 10218 | 2 4545665539 | RS8884 | ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SC02-MR1 INTERGENIC REGION [Saccharomyces cerevisiae] | other |
| 18109 | 2 4534292267 | AA188981 | Homo sapiens retinoblastoma-associated protein HEC mRNA complete cds | ? |
| 6485 | 2 4613518897 | X92098 | H. sapiens mRNA for transmembrane protein mp24 | SS, TM |
| 34954 | 2 4591845976 | AA342959 | EST - RC_AA342959 | ? |
| 42558 | 2 4588637205 | W74751 | ESTs | other |
| 27444 | 2 4585750553 | AA430160 | ESTs Weakly similar to F25H9.7 [C. elegans] | other |
| 21284 | 2 4582503599 | R10301 | EST | ? |
| 6920 | 2 4580590729 | AF006265 | Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds | other |
| 30037 | 2 4544484116 | N27439 | ESTs | TM |
| 27832 | 2 4527990177 | AA442702 | ESTs Weakly similar to W02B12.7 [C. elegans] | TM |

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|-------|--------------|----------|---|-------|
| 3290 | 2 4525517032 | S59164 | RYK receptor-like tyrosine kinase | TM |
| 25040 | 2 452352641 | AA010188 | ESTs | other |
| 37713 | 2 448700271 | AA461317 | ESTs | other |
| 40477 | 2 4477660739 | N24006 | Homo sapiens BAC clone RC300E22 from Tg21 c311 | other |
| 25382 | 2 4470532201 | H72014 | ESTs | other |
| 35521 | 2 4465885249 | AA400631 | ESTs | other |
| 20324 | 2 4464618504 | N35406 | Phospholipase C beta 4 | SS |
| 18620 | 2 4460334893 | F02506 | ESTs | other |
| 21087 | 2 4406971835 | R00186 | EST | ? |
| 9950 | 2 4398630157 | N71503 | ESTs | other |
| 31965 | 2 4363228422 | N93629 | ESTs | SS |
| 15120 | 2 4345895403 | U73524 | Human putative ATP/GTP-binding protein (HEAD) mRNA complete cds | TM |
| 28813 | 2 4330770686 | D59257 | Human C-1 mRNA complete cds | other |
| 38082 | 2 4295434916 | AA482284 | ESTs | other |
| 34723 | 2 428289395 | AA287115 | ESTs | other |
| 7960 | 2 427332569 | AA285277 | Homo sapiens brain expressed rna finger protein mRNA complete cds | other |
| 18073 | 2 4231729031 | AA160453 | EST | other |
| 36755 | 2 422243302 | AA436698 | EST - RC_AA436698 | other |
| 18927 | 2 4187841215 | F11087 | ESTs | other |
| 3457 | 2 4186224787 | S74728 | Arlequin | TM |
| 38806 | 2 4177893475 | AA598844 | ESTs | other |
| 20967 | 2 41519947 | N76086 | ESTs | other |
| 24752 | 2 4141496374 | Z40012 | Homo sapiens mRNA for KIAA0587 protein complete cds | other |
| 28443 | 2 4138974256 | AA621011 | ESTs | ? |
| 452 | 2 4135942278 | D38076 | RAN binding protein 1 | other |
| 11701 | 2 4134095351 | AA263031 | Homo sapiens RRM RNA binding protein GRY-tp (GRY- RBP) mRNA complete cds | other |
| 13655 | 2 412509306 | AA458919 | ESTs Weakly similar to 26S proteasome subunit p4 S [H sapiens] | other |
| 24822 | 2 4119068031 | Z40958 | ESTs | other |
| 12872 | 2 4112720798 | AA417067 | ESTs | other |
| 4836 | 2 4106618618 | U63717 | Human osteoclast stimulating factor mRNA complete cds | other |
| 42200 | 2 4083828799 | T83729 | EST - RC_T83729 | ? |
| 10987 | 2 4076548868 | AA132239 | ESTs Highly similar to HYPOTHETICAL 474 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae] | other |
| 35672 | 2 4073821434 | AA404995 | EST - RC_AA404995 | other |
| 6224 | 2 406310653 | X77748 | Glutamate receptor metabotropic 3 | TM |
| 28395 | 2 404213441 | AA610064 | ESTs | other |
| 36380 | 2 4032664297 | AA438291 | ESTs Weakly similar to No definition line found [C elegans] | other |
| 21045 | 2 4031905697 | N93403 | ESTs | ? |
| 4658 | 2 4024605599 | U49379 | Human diacylglycerol kinase epsilon DOK mRNA complete cds | TM |
| 12916 | 2 3998505367 | AA427745 | ESTs | other |
| 20850 | 2 3998090334 | N69514 | ESTs Weakly similar to oxidoreductase [H sapiens] | other |
| 29759 | 2 3986103066 | H99872 | ESTs | other |
| 36786 | 2 3971559161 | AA435815 | Human CLK-associated RS cytoplasm CARS-Cyp mRNA complete cds | other |
| 31942 | 2 3947415736 | N93185 | ESTs | other |
| 7097 | 2 39382714 | AA011452 | ESTs | other |
| 38462 | 2 3936147708 | D50063 | ESTs | other |
| 14420 | 2 3919915706 | AA600322 | ESTs Highly similar to AAC-RICH mRNA CLONE AAC3 PROTEIN [Drosophila melanogaster] | other |
| 34629 | 2 3916035475 | AA282527 | EST - RC_AA282527 | other |
| 27431 | 2 3905463084 | AA429038 | ESTs | TM |
| 8387 | 2 3904071666 | X85372 | H sapiens mRNA for Sm protein F | other |
| 11342 | 2 3902176276 | AA223674 | Homo sapiens mRNA for KIAA0704 protein partial cds | other |

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|-------|---------------|----------|--|-------|
| 1487 | 2 386369765 | J04608 | Topoisomerase (DNA) II alpha (170LD) | other |
| 9841 | 2 3841922016 | M5724 | Centromere autoantigen C | other |
| 11454 | 2 3820201875 | AA233854 | ESTs | TM |
| 29950 | 2 3807495489 | N24902 | Homo sapiens mRNA for E1B-55kDa-associated protein | TM |
| 8396 | 2 3807187289 | AA426176 | ESTs Weakly similar to Similar to S. cerevisiae hypothetical protein L3111 [H.sapiens] | other |
| 32978 | 2 3805956259 | W47788 | Human terminal transferase mRNA complete cds | other |
| 27872 | 2 3784145640 | AA459254 | ESTs | other |
| 11623 | 2 3769665069 | AA243617 | ESTs | other |
| 26582 | 2 3766857777 | AA273768 | ESTs | other |
| 22142 | 2 3761275301 | RS1382 | Homo sapiens mRNA for KIAA0659 protein partial cds | other |
| 13533 | 2 3759359586 | AA454607 | ESTs Highly similar to HYPOPHOSPHATE 40 2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans] | other |
| 11534 | 2 3747649776 | AA236223 | ESTs | other |
| 5576 | 2 3706287882 | X54229 | DEK PROTEIN | other |
| 6231 | 2 3660594679 | X78121 | Choroderemia | TM |
| 7382 | 2 3677644584 | M16967 | Coagulation factor V | other |
| 22887 | 2 3673034941 | T03314 | ESTs | TM |
| 24371 | 2 3603729415 | W67415 | ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens] | other |
| 25286 | 2 3656134948 | AA045261 | ESTs | other |
| 9054 | 2 3645742793 | G2472 | ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens] | other |
| 8163 | 2 3646144677 | AA327394 | ESTs | other |
| 12233 | 2 3640777711 | AA343513 | ESTs Weakly similar to LINE/hp H-chain fusion protein [M.musculus] | SS |
| 22924 | 2 3634027127 | T08195 | ESTs | other |
| 14071 | 2 361524453 | AA599219 | ESTs Moderately similar to ALR [H.sapiens] | other |
| 12401 | 2 3607293644 | AA402229 | ESTs | other |
| 26169 | 2 3599633182 | AA251069 | ESTs Weakly similar to DRF YDR261c [S.cerevisiae] | ? |
| 23065 | 2 3592943521 | T23539 | ESTs Highly similar to zinc finger protein [M.musculus] | other |
| 20524 | 2 3562118239 | N53965 | ESTs | other |
| 20837 | 2 3577032218 | N69263 | ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens] | other |
| 18201 | 2 3573132815 | AA195598 | Homo sapiens DNA sequence from PAC 434D14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydrocortisone (11-beta) Dehydrogenase 1 the ADOCA2BP adenine A2b receptor LINE pseudogene the IRF6 | other |
| 7613 | 2 3568680502 | AA248297 | ESTs | TM |
| 21195 | 2 3547018746 | R07210 | ESTs | other |
| 13377 | 2 3513919997 | AA449720 | Homo sapiens clone 24706 mRNA sequence | other |
| 9714 | 2 3497248732 | L44567 | ESTs | other |
| 41537 | 2 3460892052 | R55673 | ESTs | other |
| 17352 | 2 34595172 | AA100925 | ESTs | other |
| 19114 | 2 3446813991 | AA276907 | ESTs | ? |
| 24890 | 2 3440589932 | Z41634 | ESTs | other |
| 28796 | 2 3434466024 | D51272 | EST - RC_D51272_s | ? |
| 36798 | 2 342525534 | AA425870 | ESTs Weakly similar to B0564.1 [C.elegans] | other |
| 22491 | 2 34039294581 | R70012 | EST | other |
| 4798 | 2 3403776443 | U61538 | Human calcium-binding protein cnp mRNA complete cds | other |
| 40847 | 2 3397210586 | N66354 | ESTs | other |
| 15657 | 2 3392343806 | W03627 | Small inducible cytokine A5 (RANTES) | TM |
| 24482 | 2 3374046148 | Z36137 | ESTs | other |
| 42022 | 2 3336939603 | TS3138 | Homo sapiens mRNA for NTCF-4 | TM |
| 38233 | 2 3314220199 | AA489023 | ESTs | other |
| 41221 | 2 3310635524 | R21531 | ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens] | other |
| 8053 | 2 3297250374 | AA309860 | ESTs | other |

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|-------|--------------|----------|--|-------|
| 363 | 2.3275393529 | D26528 | Human mRNA for RNA helicase complete cds | ? |
| 26679 | 2.3241677574 | AA281733 | ESTs | other |
| 13407 | 2.3216524472 | AA450200 | ESTs | IM |
| 17955 | 2.3192657399 | AA166703 | ESTs | IM |
| 31858 | 2.3160641803 | N90680 | EST | ? |
| 24092 | 2.3151511564 | W62845 | Homo sapiens protein tyrosine phosphatase PIR1 mRNA complete cds | SS |
| 16759 | 2.3118245547 | AA046294 | ESTs | other |
| 7661 | 2.311355404 | AA252436 | Homo sapiens clone 23797 and 23917 mRNA partial cds | other |
| 41176 | 2.3111560749 | R05379 | Natural resistance-associated macrophage protein 2 | TM |
| 3660 | 2.3104353895 | U13913 | Homolog of Drosophila slowpoke (potassium channel calcium activated) | TM |
| 40986 | 2.3077403929 | N68149 | ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR (Homo sapiens) | other |
| 19428 | 2.3068982001 | H22949 | EST | ? |
| 36080 | 2.3048383557 | AA417282 | EST - RC_AA417282 | other |
| 27264 | 2.3043527378 | AA418369 | ESTs | other |
| 13600 | 2.3031966696 | AA456286 | ESTs | other |
| 13552 | 2.3028988375 | AA454943 | ESTs | other |
| 15664 | 2.3025773291 | V87456 | ESTs Moderately similar to YY1-associated factor 2 (H.sapiens) | other |
| 26583 | 2.3025403178 | AA279774 | ESTs | ? |
| 37434 | 2.3013886299 | AA454149 | EST | ? |
| 7833 | 2.2992574443 | AA249300 | ESTs | other |
| 3674 | 2.2985613315 | U06237 | Human fetal Aiz-50-reactive clone 1 (FAC1) mRNA complete cds | other |
| 33684 | 2.2984566375 | Z38770 | ESTs | other |
| 11178 | 2.2972286082 | AA167436 | ESTs | ? |
| 16977 | 2.2912855364 | AA054616 | ESTs | other |
| 19799 | 2.290119924 | H57330 | EST | ? |
| 5948 | 2.2900738182 | X63337 | EST - X63337 | ? |
| 42097 | 2.2881548729 | T66316 | isoenzyme-cRNA synthetase | ? |
| 24247 | 2.2881066691 | V073010 | Ribosomal protein L37 | other |
| 40679 | 2.2870463837 | N67816 | ESTs Moderately similar to H1 ALU SUBFAMILY SX WARNING ENTRY III (H.sapiens) | other |
| 5075 | 2.2860441014 | X59405 | Membrane cofactor protein (CD45) (prophages-lymphocyte cross-reactive antigen) | ? |
| 22325 | 2.2860330577 | R50777 | ESTs | other |
| 9621 | 2.2844572929 | J05032 | ASPARTYL-TRNA SYNTHETASE | other |
| 9239 | 2.2823045248 | D79100 | ESTs | other |
| 41997 | 2.2816672356 | T47768 | ESTs | other |
| 31105 | 2.28091752 | N63307 | EST | ? |
| 38565 | 2.2784164837 | F04320 | Replication factor C 37-kD subunit | other |
| 7404 | 2.279387256 | AA094989 | Homo sapiens voltage dependent anion channel protein mRNA complete cds | other |
| 6388 | 2.2788070475 | X85373 | H sapiens mRNA for Sm protein G | other |
| 20263 | 2.2728348551 | N31952 | ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F22A8.5 IN CHROMOSOME III (Caenorhabditis elegans) | other |
| 14529 | 2.2722894932 | AA620307 | ESTs | other |
| 21197 | 2.2718368964 | R07320 | ESTs | other |
| 28203 | 2.2692501412 | AA490069 | ESTs | other |
| 36320 | 2.2687130032 | AA490611 | ESTs | other |
| 41625 | 2.2680307053 | R69333 | ESTs | other |
| 4674 | 2.265734645 | U54999 | Human LGN protein mRNA complete cds | other |
| 26961 | 2.2637023919 | D80037 | EST Weakly similar to C90B8.3 (C.elegans) | other |
| 31062 | 2.2633860539 | N62827 | ESTs | other |
| 28756 | 2.2627797292 | AA263832 | ESTs | other |
| 11567 | 2.2614480815 | AA235747 | Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds | other |

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|-------|---------------|----------|---|--------|
| 25050 | 2 2650603659 | AA011134 | ESTs Weakly similar to rrm1 (H sapiens) | TM |
| 41935 | 2 2592192037 | T29681 | Human serine kinase mRNA, complete cds | other |
| 26895 | 2 2582367069 | AA292765 | H sapiens mRNA for M-phase phosphoprotein mpp5 | other |
| 40585 | 2 2581993468 | N34891 | Homo sapiens mRNA for KIAA0595 protein partial cds | other |
| 3343 | 2 2568482074 | M87930 | SIGNAL, TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA | other |
| 42435 | 2 2532463427 | W46594 | ESTs | ? |
| 5937 | 2 2489783488 | X62534 | High-mobility group (non-reducing chromosomal) protein 2 | other |
| 21241 | 2 2477801609 | R08617 | ESTs | TM |
| 25756 | 2 2472506561 | AA135968 | ESTs | TM |
| 34184 | 2 2459300213 | AA227959 | Human cyclinase protease Mch2 isoform alpha (Mch2) mRNA, complete cds | other |
| 8672 | 2 24506654129 | AA477046 | ESTs | other |
| 7387 | 2 2447544716 | AA293977 | ESTs | other |
| 28822 | 2 2424116577 | D59352 | ESTs | TM |
| 18216 | 2 2410305445 | AA173223 | ESTs | other |
| 20843 | 2 239268723 | N69352 | Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds | other |
| 10064 | 2 2387950133 | R10266 | ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN FRA04PAC2 INTERGENIC REGION [Saccharomyces cerevisiae] | other |
| 34094 | 2 2384154308 | AA206088 | ESTs | other |
| 41240 | 2 2380827236 | R27296 | ESTs | other |
| 22834 | 2 2346537819 | R82837 | ESTs | other |
| 19686 | 2 2319351958 | H48502 | ESTs | SS |
| 34568 | 2 23002030547 | AA280609 | ESTs Weakly similar to KC282.3 gene product [C. elegans] | other |
| 28448 | 2 2295708871 | AA621752 | Human 26S proteasome-associated pad1 homolog (POH1) mRNA, complete cds | other |
| 20909 | 2 2284835116 | N71704 | ESTs | other |
| 651 | 2 22820753259 | D78129 | EST - D78129 | SS, TM |
| 40409 | 2 2244318492 | H98977 | Homo sapiens exportin 1 mRNA, complete cds | other |
| 20340 | 2 224062627 | N38825 | ESTs | other |
| 20002 | 2 2233023284 | H93005 | EST - RC_H93005 | other |
| 37321 | 2 2209202793 | AA451898 | ESTs | other |
| 8274 | 2 2208782623 | AA20205 | ESTs | other |
| 20221 | 2 2197714612 | N29345 | ESTs | other |
| 5792 | 2 2186801223 | X54941 | CDC28 protein kinase I | other |
| 4034 | 2 21806435 | U21858 | Human transcription initiation factor TFIIID subunit TAF101 mRNA, complete cds | other |
| 36222 | 2 2149577598 | AA421481 | ESTs | other |
| 15667 | 2 2146936555 | AA031591 | ESTs | other |
| 4721 | 2 2134595068 | U58046 | Human mRNA for KIAA0129 gene, complete cds | other |
| 28656 | 2 2125017907 | D19708 | Human Gu protein mRNA, partial cds | TM |
| 20723 | 2 2113306194 | N66093 | ESTs | other |
| 6714 | 2 2062571749 | Y08612 | H sapiens mRNA for Nup88 protein | ? |
| 19240 | 2 2055683096 | H13265 | ESTs | other |
| 36447 | 2 2050764323 | AA428188 | ESTs | other |
| 11688 | 2 202443216 | AA252672 | Homo sapiens diphthamide biosynthesis protein-2 (DIPY2) mRNA, complete cds | other |
| 21650 | 2 2018153311 | R37938 | Homo sapiens KIAA0440 mRNA, partial cds | other |
| 14152 | 2 2015953698 | AA489790 | Homo sapiens Ran-GTP binding protein mRNA, partial cds | other |
| 42657 | 2 1975280207 | W92771 | GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR | other |
| 4642 | 2 1968027789 | U52427 | Human RNA polymerase II subunit hRPB7 mRNA, complete cds | ? |
| 32779 | 2 1962611079 | W02102 | ESTs | TM |
| 36341 | 2 1951559134 | AA490307 | ESTs | other |
| 11803 | 2 19201143838 | AA257971 | ESTs | other |
| 34826 | 2 190705129 | AA262677 | ESTs | TM |
| 39085 | 2 1895604523 | AA620599 | ESTs | other |

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| | | | | |
|-------|--------------|----------|---|-------|
| 4046 | 2 1877764122 | U22376 | MYB PROTO-ONCOGENE PROTEIN | ? |
| 11600 | 2 1876723705 | AQ42968 | ESTs Weakly similar to house-keeping protein (Mmusculae) | other |
| 5051 | 2 1056000566 | U76338 | Human BRCA1-associated RING domain protein (BARD1) mRNA complete cds | other |
| 33917 | 2 1864855739 | AA167323 | ESTs | TM |
| 20674 | 2 1838972155 | N63392 | ESTs | TM |
| 41031 | 2 1766902734 | N91246 | ESTs | ? |
| 25114 | 2 1759894688 | AA020923 | EST | ? |
| 24711 | 2 1758363153 | Z39645 | ESTs | other |
| 4733 | 2 1721786534 | U58658 | Human unknown protein mRNA within the p53 intron 1 complete cds | other |
| 4871 | 2 1712198791 | U55033 | Human glycican-5 (GPC5) mRNA complete cds | other |
| 29733 | 2 1687028853 | H99398 | EST | ? |
| 23155 | 2 1678113438 | T30550 | ESTs | other |
| 34638 | 2 164515923 | AQ282987 | EST | ? |
| 35541 | 2 1621480372 | AA400986 | Prothymosin alpha | other |
| 1889 | 2 1595384252 | L20591 | Annexin III (spocorin III) | ? |
| 15106 | 2 1591553363 | U58111 | PROTEIN PHOSPHATASE INHIBITOR 2 | ? |
| 40131 | 2 1583553082 | H79779 | Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds | other |
| 19516 | 2 158045763 | H20207 | EST | other |
| 4136 | 2 1577799237 | U28014 | ICH-2 PROTEASE PRECURSOR | other |
| 20276 | 2 1548737104 | N32919 | ESTs | other |
| 13292 | 2 1546700991 | AA447621 | ESTs Highly similar to 40 KD PROTEIN (Borna disease virus) | other |
| 20005 | 2 154262609 | N63165 | ESTs | other |
| 6065 | 2 1526648242 | X88560 | Sp3 transcription factor | other |
| 18238 | 2 1516362853 | AQ205389 | ESTs | other |
| 21627 | 2 1515999164 | R37410 | EST | ? |
| 3438 | 2 1502571642 | Z72024 | Eukaryotic translation initiation factor 5A | ? |
| 34648 | 2 1498935434 | AQ283772 | ACTIVATOR 1 36 KD SUBUNIT | other |
| 5964 | 2 1488964343 | X63657 | Follicular lymphoma variant translocation 1 | SS, |
| 13250 | 2 1486005975 | AA446459 | ESTs | other |
| 34370 | 2 1465845856 | AQ251029 | ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MHC2-CPY2 INTERGENIC REGION (Saccharomyces cerevisiae) | other |
| 27996 | 2 145312871 | AA470156 | ESTs Weakly similar to dyx1n 74k chain cytosolic (R.novegicus) | SS, |
| 4408 | 2 1398885247 | U41745 | Human PDGF associated protein mRNA complete cds | other |
| 4187 | 2 1395632136 | U30888 | Human tRNA-guanine transglycosylase mRNA complete cds | other |
| 10804 | 2 1368859886 | AQ069549 | ESTs | other |
| 34582 | 2 1340290702 | AQ279985 | Human mRNA for KIAA0372 gene complete cds | other |
| 18360 | 2 1331897016 | AQ227119 | ESTs | other |
| 5223 | 2 1298428563 | U83843 | EST - U53843 | other |
| 37415 | 2 1270169134 | AA453807 | EST | other |
| 14582 | 2 1260941468 | AA621340 | ESTs Weakly similar to HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION (Saccharomyces cerevisiae) | other |
| 27756 | 2 1236471107 | AA453447 | ESTs | other |
| 13787 | 2 1232866197 | AA03745 | ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 (Saccharomyces cerevisiae) | other |
| 5173 | 2 1232706565 | U81554 | Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds | other |
| 40029 | 2 1214337319 | H08221 | Human E2 Ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA complete cds | other |
| 19972 | 2 1193721042 | H83639 | ESTs | other |
| 23301 | 2 117519655 | T52847 | ESTs | other |
| 20504 | 2 1134521605 | N52366 | ESTs | other |
| 40145 | 2 1132200072 | H81391 | Human mRNA for histamine N-methyltransferase complete cds | other |
| 3461 | 2 1131164397 | S75256 | EST - S75256 | SS, |
| 41893 | 2 1124188285 | T23611 | ESTs | other |

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| | | | | |
|-------|--------------|---------------|---|--------|
| 36298 | 2 1092181318 | C14805 | EST - RC_C14805 | other |
| 36321 | 2 1084565145 | AA416676 | ESTs Weekly similar to TRANSFORMATION-SENSITIVE PROTEIN BP-53P-3521 (H sapiens) | other |
| 8362 | 2 1077405838 | AA424195 | ESTs Weekly similar to C5086.3 (C elegans) | other |
| 26288 | 2 1075593303 | AA598447 | Homo sapiens orphan 1 mRNA complete cds | other |
| 5807 | 2 1071000331 | X55740 | 5' nucleotidase (CD73) | ? |
| 15747 | 2 1051059599 | H53572 | ESTs | other |
| 38165 | 2 1052335506 | AA486777 | ESTs | TM |
| 924 | 2 1037724222 | HG1112-HT1112 | EST - HG1112-HT1112 | ? |
| 9544 | 2 1022251514 | H72630 | ESTs | other |
| 6384 | 2 1005713327 | AA424282 | Human 75-4D autoantigen (PM-Scl) mRNA complete cds | other |
| 25165 | 2 1005132784 | AA227837 | Rattus pigmentosa 3 (X-linked recessive) | SS, TM |
| 24348 | 2 1003556938 | W85403 | Tropomyosin alpha chain (skeletal muscle) | ? |
| 41401 | 2 0994968367 | R43334 | Homo sapiens KIAA0410 mRNA complete cds | other |
| 35340 | 2 0993752592 | AA398900 | EST - RC_AA398900 | other |
| 10698 | 2 0990741816 | AA112063 | ESTs Weekly similar to PRE-MRNA SPLICING HELICASE SBP2 (S cerevisiae) | other |
| 381 | 2 0974305874 | D28473 | Isoleucine-tRNA synthetase | other |
| 22051 | 2 0871755 | R49497 | ESTs Weekly similar to RPLU SUBFAMILY J WARNING ENTRY III (H sapiens) | other |
| 3293 | 2 086563118 | N34693 | Testis specific protein Y-ward | TM |
| 11528 | 2 0854548212 | AA236018 | ESTs Weekly similar to unknown (S cerevisiae) | ? |
| 11890 | 2 0852665665 | AA278323 | Homo sapiens clone 24606 mRNA sequence | TM |
| 13643 | 2 0852581265 | AA455578 | Homo sapiens clone 24477 mRNA sequence | other |
| 19927 | 2 0852547855 | H71829 | ESTs | other |
| 36511 | 2 0827895929 | AA429632 | ESTs | ? |
| 2130 | 2 0825292202 | L40407 | Homo sapiens thyroid receptor interactor (TRIP9) gene complete cds | ? |
| 7193 | 2 0824070677 | AA040768 | Homo sapiens clone TJAB C1-cu-chat region mRNA | TM |
| 5448 | 2 0821543167 | X02751 | Neuroblastoma RAS viral (v-ras) oncogene homolog | ? |
| 35956 | 2 0815768183 | AA412533 | ESTs | other |
| 7526 | 2 0810133692 | AA149259 | ESTs | other |
| 39592 | 2 0802891765 | F09351 | ESTs Weekly similar to weakly similar to S cerevisiae PTM1 precursor (C elegans) | TM |
| 28029 | 2 0855738844 | AA478479 | ESTs | other |
| 18425 | 2 0855157851 | AA232103 | ESTs | other |
| 23494 | 2 0843300602 | T70045 | ESTs Weekly similar to HYPOTHETICAL 33.2 KD PROTEIN F26A3.7 IN CHROMOSOME I (C elegans) | other |
| 30082 | 2 0840312831 | N56900 | EST | ? |
| 32597 | 2 0839196473 | T47333 | Human TP43 subunit TAF155 (TAF155) mRNA complete cds | other |
| 33368 | 2 0838178514 | W80614 | ESTs | other |
| 10259 | 2 0829121213 | R77527 | ESTs | other |
| 21892 | 2 0825457608 | R43305 | ESTs | other |
| 20590 | 2 0820571859 | N58146 | ESTs | other |
| 12907 | 2 0807802388 | AA427577 | ESTs | other |
| 22858 | 2 0773089407 | T16264 | ESTs | other |
| 42044 | 2 0752746251 | T58753 | ESTs | other |
| 4210 | 2 0750374179 | U31814 | Human transcriptional regulator homolog RPD3 mRNA complete cds | other |
| 39 | 2 074214715 | AB003606 | Homo sapiens mRNA for Cdc7-related kinase complete cds | other |
| 14350 | 2 0739236064 | A4598831 | ESTs | TM |
| 29840 | 2 0729224128 | N21600 | ESTs | other |
| 25593 | 2 0715918096 | AA113149 | Homo sapiens IPL (IPL) mRNA complete cds | other |
| 20071 | 2 0708411247 | AA236880 | Protein phosphatase 2A regulatory subunit B' alpha-1 | other |
| 25529 | 2 0699045563 | AA275594 | EST | ? |
| 12154 | 2 0692192056 | AA291293 | ESTs | other |
| 18817 | 2 0694614007 | F10077 | ESTs | ? |

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| | | | | |
|-------|--------------|----------|--|-------|
| 6635 | 2 0674931973 | X99505 | H sapiens mRNA for SM73B protein | other |
| 6661 | 2 066065203 | Y00271 | Phosphorylase kinase subunit 2 | other |
| 22077 | 2 0647745388 | R49482 | ESTs | other |
| 11752 | 2 0645929355 | AA256042 | ESTs | other |
| 41257 | 2 0634413934 | R31640 | ESTs | SS |
| 6904 | 2 0622381932 | Z34597 | Histamine receptor H1 | TM |
| 16879 | 2 060262971 | AA056538 | ESTs | other |
| 38340 | 2 0595449295 | AA481403 | ESTs | other |
| 4111 | 2 0567636707 | U26312 | Human heterochromatin protein HP1Hs-gamma mRNA complete cds | other |
| 32878 | 2 0545812272 | V037448 | ESTs | TM |
| 21743 | 2 0543668446 | R40576 | ESTs Moderately similar to H1 ALU SUBFAMILY SX WARNING ENTRY #H (H sapiens) | ? |
| 25968 | 2 0525018401 | AA234935 | ESTs | other |
| 24559 | 2 0506511896 | Z39211 | Homo sapiens GDP-L-fucose pyrophosphorylase (GFP) mRNA complete cds | other |
| 30030 | 2 0505994824 | AA461148 | ESTs | other |
| 61 | 2 0484705331 | AC002115 | Cytochrome c oxidase subunit VIb | ? |
| 6306 | 2 0474040935 | X81625 | ELKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 | ? |
| 8203 | 2 0473464771 | AA382517 | EST - AA302517 | other |
| 34357 | 2 0459036477 | AA251430 | ESTs Highly similar to RAS-RELATED PROTEIN RAB-10 [Cans familiens] | other |
| 36972 | 2 0450599742 | AA427867 | Tyrosine 3-monooxygenase/tyrosinase 6: monooxygenase activation protein beta polypeptide | other |
| 28156 | 2 0459278063 | AA490057 | H sapiens mRNA for nuclear protein SA-2 | ? |
| 24434 | 2 045695222 | V92787 | ESTs | other |
| 33508 | 2 0449481783 | V68772 | Human DNA sequence from cosmid FO811 on chromosome 6. Contains Daxo BING1 Tapase RGL2 KEX BING4 BING5 ESTs and CpG islands | other |
| 37681 | 2 0449346104 | AA460675 | H sapiens mRNA for TRES | other |
| 27125 | 2 0448698236 | AA405505 | Homo sapiens mRNA for putative RNA helicase 3' and | other |
| 3780 | 2 0445300702 | U06051 | Zinc finger protein 148 (p4Z-52) | other |
| 9112 | 2 0443525757 | D16611 | Coproporphyrinogen oxidase (coproporphyrin haldroporphyrin) | TM |
| 8357 | 2 044244223 | AA418921 | ESTs Highly similar to RSPS PROTEIN [Saccharomyces cerevisiae] | other |
| 9133 | 2 0436113204 | D30946 | ESTs Highly similar to TRANSLOCAN-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus] | TM |
| 7519 | 2 0414123824 | AA147425 | EST - AA147425_s | other |
| 14701 | 2 0413756305 | D16324 | ESTs | other |
| 380 | 2 0411436076 | D28423 | EST - D28423 | ? |
| 30571 | 2 0348528604 | N49595 | ESTs | other |
| 825 | 2 0329522889 | D73226 | Homocarbonylase synthetase (barn:propionyl-Coenzyme A-carboxylase (ATP-hydrolyzing)) ligase | TM |
| 27744 | 2 0318041265 | AA452819 | ESTs Weakly similar to HYPOTHETICAL PROTEIN H0034 [Haemophilus influenzae] | other |
| 3997 | 2 0311208335 | U19906 | Angiogenin vasopressin receptor 1 (AVPR1) | ? |
| 22717 | 2 0302732387 | R91394 | EST - RC_R91394 | ? |
| 377 | 2 0289078264 | D28364 | EST - D28364 | other |
| 28581 | 2 0274006652 | C21163 | EST | ? |
| 11790 | 2 0269672127 | AA256878 | ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae] | other |
| 37931 | 2 0269058272 | AA478523 | ESTs Weakly similar to H1 ALU SUBFAMILY J | other |
| 24678 | 2 0209819539 | Z39349 | ESTs Weakly similar to NUCLEAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae] | other |
| 10940 | 2 0209035614 | AA122217 | ESTs Weakly similar to HYPOTHETICAL 613 KD PROTEIN F35B5.5 IN CHROMOSOME III [C. elegans] | ? |
| 13964 | 2 0207516872 | AA479048 | ESTs | TM |
| 15665 | 2 019773566 | V67631 | Homo sapiens clone 24538 mRNA sequence | ? |
| 28379 | 2 0189373185 | AA609710 | ESTs | other |
| 13349 | 2 0172119305 | AA493269 | ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa] | SS. |
| 7322 | 2 0167797545 | AA002692 | ESTs Weakly similar to the KIAA2138 gene product is novel [H sapiens] | other |
| 29358 | 2 0165296752 | H70641 | EST - RC_H70641 | ? |

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| | | | | |
|-------|--------------|----------|--|-------|
| 24230 | 2 016017562 | W72276 | ESTs | other |
| 40212 | 2 0158778189 | H88535 | Human clone 121711 defective manner transposon | ? |
| 729 | 2 015733779 | D63778 | Human mRNA sequence | other |
| 17951 | 2 0144767235 | AA165526 | Human mRNA for KIAA0194 gene partial cds | other |
| 33943 | 2 0135799277 | AA171739 | Homo sapiens bifunctional ATP sulfurylase/adenosine 5'-phosphosulfate kinase mRNA complete cds | other |
| 5676 | 2 0118426199 | X59244 | ESTs | other |
| 36319 | 2 0116526739 | AA425107 | Zinc finger protein 43 (HTF6) | other |
| 25654 | 2 0097423819 | AA126951 | ESTs Weakly similar to DNA directed RNA polymerase [D motuogaster] | other |
| 16344 | 2 0090457727 | AA018907 | ESTs | ? |
| 8118 | 2 0090099575 | AA328993 | ESTs | other |
| 29952 | 2 0087628098 | N25228 | ESTs | TM |
| 32236 | 2 0079250736 | R49327 | Neutral resistance-associated macrophage protein 2 | TM |
| 3279 | 2 0072427596 | M94065 | DIIHYDROXYFATE DE-HYDROGENASE PRECURSOR | TM |
| 18255 | 2 0065069683 | AA013349 | ESTs | other |
| 37972 | 2 0059209236 | AA479215 | EST - RC_AA479215 | TM |
| 41256 | 2 005658644 | R31577 | ESTs | other |
| 34834 | 2 0050133743 | AA292655 | ESTs | other |
| 23189 | 2 0039279023 | T33215 | ESTs | other |
| 29851 | 2 0034762995 | N22145 | ESTs | other |
| 32802 | 2 | W02519 | EST | ? |

FIGURE 8 (cont.)

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| New Key Number | Accession | fold upregulated of Tumor over normal colon | Unigene Descriptor | |
|----------------|-----------|---|---|--------|
| 104660 | AA007160 | 23 | ESTs | SS |
| 130016 | AA055811 | 14 | transmembrane glycoprotein | SS, TM |
| 104954 | AA074514 | 10 | ESTs; Moderately similar to (define not available 4753768) [H.sapiens] | Other |
| 105082 | AA143763 | 7 | ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans] | Other |
| 109141 | AA176428 | 7 | ESTs | Other |
| 108893 | AA135894 | 6 | retinoic acid induced 3 | TM |
| 108927 | AA143493 | 5 | ESTs; Weakly similar to PLECKSTRIN [H.sapiens] | Other |
| 109027 | AA157818 | 5 | Human endogenous retroviral protease mRNA; complete cds | Other |
| 133015 | AA047036 | 4 | ESTs | Other |
| 114546 | AA056263 | 4 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | Other |
| 104974 | AA085918 | 4 | H.sapiens HUNK1 mRNA | Other |
| 108695 | AA121315 | 4 | ESTs | SS |
| 105049 | AA132554 | 4 | ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens] | Other |
| 133834 | AA147510 | 4 | Homo sapiens serine protease mRNA; complete cds | Other |
| 109244 | AA194237 | 4 | ESTs; Weakly similar to C17H11.6 [C.elegans] | Other |
| 128411 | AA007555 | 3 | ESTs; Weakly similar to transformation-related protein [H.sapiens] | SS, TM |
| 114508 | AA043551 | 3 | ESTs | Other |
| 104888 | AA053660 | 3 | ESTs | Other |
| 114542 | AA055768 | 3 | ESTs | SS |
| 132718 | AA056731 | 3 | Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro) | Other |
| 104953 | AA074157 | 3 | ESTs | Other |
| 132784 | AA099589 | 3 | GDP dissociation inhibitor 2 | Other |
| 130962 | AA102051 | 3 | transmembrane 4 superfamily member 6 | SS, TM |
| 134421 | AA122386 | 3 | collagen; type V; alpha 2 | SS |
| 105035 | AA128486 | 3 | ESTs | Other |
| 105039 | AA130349 | 3 | ESTs | Other |
| 105062 | AA134968 | 3 | ESTs | Other |
| 133617 | AA148318 | 3 | Human mRNA for KIAA0069 gene; partial cds | TM |

FIGURE 9

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| | | | | |
|--------|----------|---|---|-------|
| | | | ESTs; Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN | |
| 130335 | AA156499 | 3 | [H.sapiens] | Other |
| 105132 | AA159501 | 3 | HBV associated factor | Other |
| 109042 | AA159525 | 3 | ESTs | Other |
| 109043 | AA159605 | 3 | ESTs | Other |
| 132669 | AA188378 | 3 | ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 [H.sapiens] | Other |
| 135398 | AA194075 | 3 | nuclear receptor coactivator 4 | Other |
| 109344 | AA213696 | 3 | ESTs | SS |
| 133221 | AA235289 | 3 | ESTs; Highly similar to rap2 gene product [H.sapiens] | Other |
| 114496 | AA035611 | 2 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens] | Other |
| 128635 | AA043959 | 2 | tropomyosin 4 | Other |
| 129912 | AA047344 | 2 | ESTs; Weakly similar to similar to WW/rsp5/WWP domain containing proteins [C.elegans] | Other |
| 104927 | AA058855 | 2 | ESTs | SS |
| 132621 | AA070724 | 2 | CD44 antigen (homing function and Indian blood group system) | Other |
| 108409 | AA075578 | 2 | "zm88h3.s1 Stratagene ovarian cancer (#537219) Homo sapiens cDNA clone IMAGE:54545 3', mRNA sequence" | Other |
| 133621 | AA076138 | 2 | H2A histone family, member Y | Other |
| 108565 | AA085342 | 2 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | TM |
| 104977 | AA088228 | 2 | ESTs | Other |
| 103777 | AA093131 | 2 | Homo sapiens PAC clone DJ0167F23 from 7p15 | Other |
| 108849 | AA112540 | 2 | ESTs | Other |
| 114692 | AA121995 | 2 | ESTs; Weakly similar to Similar to potassium channel protein [C.elegans] | Other |
| 105063 | AA134985 | 2 | ESTs | Other |
| 133273 | AA147725 | 2 | dendritic cell protein | Other |
| 128515 | AA149044 | 2 | ESTs; Highly similar to the KIAA0195 gene is expressed ubiquitously [H.sapiens] | SS |
| 105182 | AA191014 | 2 | ESTs; Weakly similar to Ydr372cp [S.cerevisiae] | Other |
| 109277 | AA196332 | 2 | ESTs | Other |
| 132606 | AA199588 | 2 | ARP3 (actin-related protein 3; yeast) homolog | Other |
| 109380 | AA219015 | 2 | ESTs | Other |
| 130800 | AA223366 | 2 | ESTs; Weakly similar to katanin p80 subunit [H.sapiens] | Other |
| 129945 | AA232104 | 2 | ESTs; Highly similar to (define not available 4929579) [H.sapiens] | Other |
| 105305 | AA233609 | 2 | spindle pole body protein | Other |

FIGURE 9

(Cont.)

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| | | | |
|--------|----------|--|-------|
| 128924 | AA234962 | 2 ESTs | TM |
| 114895 | AA236177 | 2 Homo sapiens mRNA for KIAA0887 protein; partial cds | Other |

FIGURE 9 (Cont.)

FIGURE 10
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| 1 | A | B | C | D | E |
|----|--|------|----------|--|-------|
| 2 | Human alpha satellite and satellite 3 junction DNA sequence | 52.6 | M21305 | Human alpha satellite and satellite 3 junction DNA sequence | ? |
| 3 | ESTs: Weakly similar to serine protease [H sapiens] | 7.4 | AA115002 | ESTs: Weakly similar to serine protease [H sapiens] | ? |
| 4 | ESTs: Weakly similar to osteoblast specific factor 2 (OSF-2os) | 7 | D13666 | ESTs: Weakly similar to osteoblast specific factor 2 (OSF-2os) | SS |
| 5 | ESTs: Weakly similar to heat shock protein hsp41 homolog [H sapiens] | 6.8 | AA102500 | ESTs: Weakly similar to heat shock protein hsp41 homolog [H sapiens] | TM |
| 6 | ESTs | 6.2 | AA453783 | ESTs | TM |
| 7 | ESTs | 6.2 | F13673 | ESTs | other |
| 8 | ESTs: Weakly similar to nuclear protein SA-2 | 5.2 | AA106507 | ESTs: Weakly similar to nuclear protein SA-2 | ? |
| 9 | ESTs: Weakly similar to regulated collagen | 5.6 | AA106507 | ESTs: Weakly similar to regulated collagen | other |
| 10 | ESTs: Weakly similar to collagen, type I, alpha 2 | 5.4 | AA125114 | ESTs: Weakly similar to collagen, type I, alpha 2 | other |
| 11 | ESTs | 5 | Z74616 | ESTs | SS |
| 12 | ESTs | 4.7 | AA236200 | ESTs | SS |
| 13 | ESTs | 4.5 | AA291520 | ESTs | other |
| 14 | ESTs | 4.4 | V46810 | HMT1 (mRNP methyltransferase; S. cerevisiae) like 2 | other |
| 15 | ESTs | 4.3 | AA353804 | H beta 5.5 homolog | other |
| 16 | ESTs | 4.2 | R79362 | ESTs | other |
| 17 | ESTs | 4.2 | AA112012 | lactate dehydrogenase A | TM |
| 18 | ESTs | 4.1 | R92994 | matrix metalloproteinase 12 (macrophage elastase) | SS |
| 19 | ESTs | 4.1 | T32108 | ESTs | SS |
| 20 | ESTs | 4 | R71092 | TFAR18 novel apoptosis-related gene | other |
| 21 | ESTs | 4 | N32566 | ESTs: Weakly similar to Yid-330p [S. cerevisiae] | other |
| 22 | ESTs | 3.9 | C14037 | ESTs: Weakly similar to Yid-330p [S. cerevisiae] | ? |
| 23 | ESTs | 3.8 | H98655 | Homo sapiens gene for NBS1, complete cds | TM |
| 24 | ESTs | 3.8 | AA449417 | Homo sapiens mRNA for putative glucosyltransferase, partial cds | TM |
| 25 | ESTs | 3.8 | D51276 | STAT3RIN | TM |
| 26 | ESTs | 3.7 | H10353 | ESTs | other |
| 27 | ESTs | 3.7 | X03486 | H4 histone family, member G | ? |
| 28 | ESTs | 3.5 | AA453843 | ESTs: Highly similar to TSP-5 PROTEIN (Saccharomyces cerevisiae) | other |
| 29 | ESTs | 3.5 | N31700 | ESTs: Highly similar to TSP-5 PROTEIN (Saccharomyces cerevisiae) | other |
| 30 | ESTs | 3.5 | AA226672 | ESTs: Weakly similar to PES7 [H sapiens] | other |
| 31 | ESTs | 3.4 | D38567 | Human mRNA for calpastatin, complete cds | other |
| 32 | ESTs | 3.4 | AA186897 | ESTs | TM |
| 33 | ESTs | 3.4 | AA421562 | Homo sapiens secreted cement gland protein XAG-2 homolog (PAG-2IR) | SS |
| 34 | ESTs | 3.4 | V45728 | ESTs: Highly similar to HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN, type 1, alpha 2 | other |
| 35 | ESTs | 3.3 | J03464 | collagen, type I, alpha 2 | SS |
| 36 | ESTs | 3.3 | AA027066 | ESTs | SS |
| 37 | ESTs | 3.3 | R51309 | calpain-2 | other |
| 38 | ESTs | 3.3 | C21242 | calpain-2 | other |
| 39 | ESTs | 3.2 | M29540 | CARCINOEMBRYONIC ANTIGEN PRECURSOR | TM |
| 40 | ESTs | 3.2 | AA440066 | ESTs | TM |
| 41 | ESTs | 3.2 | H83742 | catechol-O-methyltransferase | other |
| 42 | ESTs | 3.1 | R56183 | ubiquitin-conjugating enzyme E2-17 KD | other |
| 43 | ESTs | 3.1 | AA043553 | ESTs: Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD | other |
| 44 | ESTs | 3.1 | AA164643 | ESTs: Weakly similar to K-167 intracellular antigen [H sapiens] | other |

FIGURE 10 (CONT)

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| A | B | C | D | E |
|----|-------|----------|--|--------|
| 45 | 26304 | A0213287 | ESTs, Weakly similar to PEANUT PROTEIN [Arachis sativa] | other |
| 46 | 27565 | A0408542 | ESTs | other |
| 47 | 10944 | A0100719 | non-specific cross reacting antigen | other |
| 48 | 11568 | A0232104 | ESTs | other |
| 49 | 17389 | A0121315 | ESTs | other |
| 50 | 17415 | A0122386 | "Collagen, type V, alpha 2" | ? |
| 51 | 23712 | T92735 | ESTs | TM |
| 52 | 25331 | A0070947 | topomycin 4 | other |
| 53 | 25358 | A0076136 | histone macroH2A1.2 | other |
| 54 | 27039 | A0406145 | ESTs | SS, TM |
| 55 | 27261 | A0425544 | Homo sapiens clone Z3659 mRNA, complete cds | other |
| 56 | 26795 | D09446 | SFRS protein kinase 1 | other |
| 57 | 32192 | R62725 | collagen, type XI, alpha 1 | other |
| 58 | 3063 | M73349 | transforming growth factor, beta-induced, 68kD | SS |
| 59 | 5219 | X00700 | collagen, type III, alpha 1 (Ellis-Danlos syndrome type IV, autosomal do | other |
| 60 | 5562 | X12876 | keratin 18 | other |
| 61 | 11618 | A0251902 | Homo sapiens lysophosphatase (LPL) mRNA, complete cds | other |
| 62 | 17686 | A0147725 | Homo sapiens GAT1 protein mRNA, complete cds | other |
| 63 | 18074 | A0188376 | ESTs, highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus] | other |
| 64 | 18074 | N95833 | ESTs | TM |
| 65 | 13612 | A0157818 | ESTs, highly similar to Gelatin not available 4127153 [H. sapiens] | other |
| 66 | 17769 | A0157818 | ESTs, highly similar to Gelatin not available 4127153 [H. sapiens] | other |
| 67 | 25544 | A0075182 | Syngene syndrome antigen 22 [Rat, homozygous protein subunit] SS-A/R | other |
| 68 | 25633 | A0131162 | ESTs | other |
| 69 | 32170 | R61297 | eukaryotic translation initiation factor 3, subunit 6 (48kD) | other |
| 70 | 33566 | Z36556 | customer protein complex, subunit alpha | SS |
| 71 | 2396 | M18728 | non-specific cross reacting antigen | other |
| 72 | 3251 | M93036 | membrane component, chromosomal 4, surface marker (35kD glycoprotein | other |
| 73 | 8150 | A0372630 | Homo sapiens GW112 protein (GW112) mRNA, complete cds | other |
| 74 | 9207 | D78052 | ESTs; highly similar to PROTEIN TRANSPORT PROTEIN SECRET GAMM | other |
| 75 | 15051 | U84661 | Human poly(d)-binding protein processed pseudogene3 | ? |
| 76 | 15614 | W83627 | ESTs; Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY III | TM |
| 77 | 25323 | A0070485 | Homo sapiens clone Z3667 unknown mRNA, partial cds | other |
| 78 | 25329 | A0070627 | ESTs; Weakly similar to KIAA18 [H. sapiens] | TM |
| 79 | 25439 | A0127058 | ESTs; Weakly similar to predicted using Genefinder [C. elegans] | TM |
| 80 | 25584 | A0131165 | heterogeneous nuclear ribonucleoprotein A2/B1 | other |
| 81 | 27468 | A0441971 | Homo sapiens mRNA for KIAA84 protein, complete cds | TM |
| 82 | 28712 | R31180 | ESTs | ? |
| 83 | 34372 | A048991 | Homo sapiens chaperonin containing 1-complex polypeptide 1, beta subunit | other |
| 84 | 34467 | A048991 | Homo sapiens chaperonin containing 1-complex polypeptide 1, beta subunit | other |
| 85 | 34921 | F099714 | 18S rRNA, 5S rRNA, 5.8S rRNA, 5.8S rRNA, 5.8S rRNA, 5.8S rRNA | other |
| 86 | 3768 | U85567 | glyceraldehyde 3-phosphate dehydrogenase | TM |
| 87 | 8592 | C00038 | ESTs | other |
| 88 | 12578 | A0431191 | ESTs | other |

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| | A | B | C | D | E |
|-----|-------|-----|----------|--|-------|
| 69 | 17627 | 2.6 | A133694 | "Homo sapiens putative G protein-coupled receptor (RARG1; Retinoic acid i | TM |
| 50 | 20752 | 2.6 | N68821 | EST1a, Weakly similar to neogline [H sapiens] | TM |
| 51 | 24534 | 2.6 | 117185 | EST1a | TM |
| 92 | 321 | 2.6 | A116161 | EST1a | other |
| 93 | 24538 | 2.6 | A116161 | proteasome (prosome, macropain) 26S subunit, non-ATPase; 11 | other |
| 94 | 26868 | 2.6 | A116879 | EST1a, Moderately similar to ubiquitin (TPR motif, Y fold) [H sapiens] | other |
| 95 | 26705 | 2.6 | A140062 | EST1a, Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE | other |
| 96 | 33583 | 2.6 | A140062 | EST1a, Moderately similar to ubiquitin (TPR motif, Y fold) [H sapiens] | other |
| 97 | 37363 | 2.6 | Z145409 | EST1a, Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE | other |
| 98 | 37170 | 2.6 | A445551 | EST1a, Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE | other |
| 99 | 35710 | 2.6 | C4524 | EST1a, Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE | other |
| 35 | 35251 | 2.6 | D05002 | EST1a, Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE | other |
| 100 | 2767 | 2.6 | M57943 | "HUMS372 Human gamma globin; Homo sapiens cDNA, clone pm734.3, 4 | SS TM |
| 101 | 5468 | 2.6 | X04347 | A04, human family member 2 | other |
| 102 | 9743 | 2.5 | D82348 | heterogeneous nuclear ribonucleoprotein A1 | other |
| 103 | 14781 | 2.5 | 135725 | Homo sapiens mRNA for 5,6-dimethyl-4-carboxamide-L-lysine-D-iso | other |
| 104 | 14804 | 2.5 | 148105 | EST1a, Highly similar to HYPOPHOSPHATE 4.2 KD PROTEIN IN SODIUM | other |
| 105 | 16874 | 2.5 | A070724 | erythrocytic translation initiation factor 3, subunit 3 (gamma, AG) | other |
| 106 | 20031 | 2.5 | N21085 | CD44 antigen (forming function and Indian blood group system) | other |
| 107 | 25464 | 2.5 | A1125679 | Homo sapiens androgen receptor associated protein | TM |
| 108 | 26830 | 2.5 | A0347359 | EST1a, Weakly similar to alternatively spliced product using exon 13A [H sa | SS |
| 109 | 26868 | 2.5 | A0490212 | lysosome (renal amyloidosis) | SS |
| 110 | 30071 | 2.5 | N30111 | histone macroH2A1.2 | other |
| 111 | 32740 | 2.5 | N30111 | replication protein A3 (14kD) | other |
| 112 | 35870 | 2.5 | V01600 | von Hippel-Lindau syndrome | other |
| 113 | 41908 | 2.5 | A416765 | heterogeneous nuclear ribonucleoprotein A1 | other |
| 114 | 4201 | 2.5 | T59161 | Thymosin, beta 1 | TM |
| 115 | 8201 | 2.4 | X66401 | proteasome (prosome, macropain) subunit, beta type 9 (large multifunctio | ? |
| 116 | 8218 | 2.4 | D30379 | EST1a, Weakly similar to NADH:UBIQUINONE OXIDOREDUCTASE (CH | other |
| 117 | 10353 | 2.4 | D79891 | EST1a | TM |
| 118 | 11067 | 2.4 | R27993 | EST1a, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOSOLIC (| other |
| 119 | 11646 | 2.4 | R24211 | DEK gene | other |
| 120 | 11946 | 2.4 | A115901 | EST1a, Moderately similar to RBOCK2 [R nonspliced] | other |
| 121 | 12767 | 2.4 | A232269 | EST1a, Weakly similar to similar to Yeast hypoxanthine protein 1.8 t67.12 like | other |
| 122 | 13772 | 2.4 | A246448 | EST1a, Weakly similar to uroporphomogen III synthase, UROHIS [H sapien | SS |
| 123 | 16728 | 2.4 | A053102 | EST1a, Weakly similar to alternatively spliced product using exon 13A [H sa | other |
| 124 | 17774 | 2.4 | A1159243 | EST1a, Highly similar to (define not available 412713) [H sapien] | SS TM |
| 125 | 21386 | 2.4 | R24509 | EST1a, Weakly similar to (define not available 412713) [H sapien] | other |
| 126 | 25433 | 2.4 | A009589 | GFP dissociation inhibitor 2 | other |
| 127 | 25603 | 2.4 | A1132032 | Homo sapiens CAGH1a (C-ACH1) mRNA, partial cds | TM |
| 128 | 25781 | 2.4 | A1119980 | ELK1, motif kinase | other |
| 129 | 26753 | 2.4 | A4352627 | EST1a | other |
| 130 | 26852 | 2.4 | A4353327 | EST1a, Weakly similar to TLS-associated protein 1A (SP1 [H sapien] | other |
| 131 | 27122 | 2.4 | A1161677 | EST1a | other |
| 132 | 28365 | 2.4 | C14090 | actin, gamma 1 | other |

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FIGURE 10 (CONT)

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| A | B | C | D | E |
|-----|-------|----------|---|--------|
| 133 | 28626 | D25560 | Home sapiens DNA from chromosome 19, contig R3379 containing USF2 | other |
| 134 | 28687 | D51241 | Home sapiens mRNA for putative vicular protein A1Pa membrane sect | SS, TM |
| 135 | 29850 | N24968 | vacuolar H(+)-ATPase subunit | other |
| 136 | 32692 | W45457 | ESTs: Moderately similar to neuronal threat protein ADIC-NTP (H sapiens) | other |
| 137 | 33811 | AA173143 | heterogeneous nuclear ribonucleoprotein G | other |
| 138 | 40721 | H93492 | ESTs: Highly similar to vlin (H sapiens) | other |
| 139 | 40741 | H94077 | ESTs: Moderately similar to putative G-binding protein (H sapiens) | other |
| 140 | 40767 | H95237 | collet, type XI, alpha 1 | other |
| 141 | 446 | D38073 | immunosome maintenance deficient (S. cerevisiae) 3 | other |
| 142 | 3350 | S81914 | DIFFERENTIATION-DEPENDENT GENE 2 | other |
| 143 | 3350 | AA252436 | Home sapiens lysophospholipase (LPL) mRNA; complete cds | other |
| 144 | 10858 | AA121819 | protease (protease, macropain) acidic, beta type 9 large multifunction | other |
| 145 | 10985 | AA121819 | ESTs: Highly similar to CTTOSOL ALKINOPEPTIDASE (Bos taurus) | other |
| 146 | 11015 | AA113750 | ESTs: Highly similar to S. Ponce BEAN/IGUS suppressor (C | other |
| 147 | 11895 | AA279420 | ESTs: Highly similar to (Genbank accession 431725) (H sapiens) | TM |
| 148 | 13366 | AA451676 | ESTs: Highly similar to (Genbank accession 431725) (H sapiens) | other |
| 149 | 14664 | W02391 | proliferation-associated 25c4, 3M0 | other |
| 150 | 17619 | AA135606 | ESTs | other |
| 151 | 18225 | AA123696 | ESTs | other |
| 152 | 20450 | N53927 | ESTs: Weakly similar to phenylalanine binding protein (H sapiens) | 2 |
| 153 | 25308 | AA065227 | ESTs: Weakly similar to coded for by C. elegans CHNA A1.c1.3 (C. elegans) | other |
| 154 | 26590 | AA382151 | ESTs: Weakly similar to predicted using GeneFinder (C. elegans) | other |
| 155 | 27624 | AA452112 | Home sapiens mRNA for putative thymosin-like protein | other |
| 156 | 27792 | AA460359 | ESTs: Weakly similar to DNA-DIRECTED RNA POLYMERASE II 14 KD P | ? |
| 157 | 28231 | AA600153 | DEK gene | other |
| 158 | 28722 | D59711 | ESTs | other |
| 159 | 30363 | N47866 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 4kD) | other |
| 160 | 32928 | W47620 | ESTs: Weakly similar to reverse transcriptase related protein (H sapiens) | other |
| 161 | 36585 | H11320 | Home sapiens IIRHFB215 mRNA; partial cds | TM |
| 162 | 40173 | H86655 | peroxylproyl isomerase E (cyclophilin B) | other |
| 163 | 40173 | N26991 | ESTs: Highly similar to (Genbank accession 427914) (H sapiens) | other |
| 164 | 40733 | W04742 | ESTs: Weakly similar to 25 kDa trypsin inhibitor (H sapiens) | other |
| 165 | 4918 | H81697 | homologous to Drosophila 1 | ? |
| 166 | 5165 | H81697 | GRAVIN | other |
| 167 | 12242 | AA372018 | ESTs | other |
| 168 | 13154 | AA442768 | Home sapiens inner mitochondrial membrane translocase Tm23 (Tm23) | ? |
| 169 | 14276 | AA598450 | ESTs | other |
| 170 | 15721 | W65348 | ESTs | TM |
| 171 | 20588 | N62945 | Home sapiens TM18A1b mRNA; complete cds | TM |
| 172 | 24021 | W42957 | ESTs | other |
| 173 | 24250 | W84712 | calumenin | SS |
| 174 | 26245 | AA050768 | ESTs | SS |
| 175 | 25430 | AA099429 | SPLICING FACTOR U2AF 35 KD SUBUNIT | TM |
| 176 | 25562 | AA128904 | heterogeneous nuclear ribonucleoprotein U (scalloid attachment factor A) | other |

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FIGURE 10 (CONT)

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| | A | B | C | D | E |
|-----|-------|-----|-----------|---|--------|
| 177 | 28745 | 2,2 | D60485 | caldesmon 1 | other |
| 178 | 31997 | 2,2 | R20669 | tumor rejection antigen (gp96) 1 | other |
| 179 | 32491 | 2,2 | T47333 | Human TFIIID subunit TAF155 (TAF155) mRNA, complete cds | other |
| 180 | 32636 | 2,2 | T93807 | high-mobility group (nonhistone chromosomal) protein 1 | other |
| 181 | 37703 | 2,2 | AA176237 | ESTs; Weakly similar to uroporphomogen III synthase, URQIIIS [H.sapien] | TM |
| 182 | 215 | 2,1 | D15627 | Human mRNA for KIAA2 gene; complete cds | TM |
| 183 | 2449 | 2,1 | M21259 | small nuclear ribonucleoprotein polypeptide E | ? |
| 184 | 3205 | 2,1 | M88458 | ER LUMEN PROTEIN RETAINING RECEPTOR 2 | TM |
| 185 | 4197 | 2,1 | U31566 | E2F transcription factor 5; p13-binding | other |
| 186 | 4811 | 2,1 | U62962 | eukaryotic translation initiation factor 3, subunit 6 (48U) | other |
| 187 | 5417 | 2,1 | X01060 | transient receptor (TP; CD71) | TM |
| 188 | 5534 | 2,1 | X01060 | transient receptor (TP; CD71) | SS, TM |
| 189 | 6535 | 2,1 | X09133 | NEUROSPIN, A GELATINASE-ASSOCIATED UROCANIC ACID RECEPTOR | other |
| 190 | 6941 | 2,1 | AA024432 | ESTs; Highly similar to KIR4A9 gene; partial cds | other |
| 191 | 10471 | 2,1 | AA143318 | Human mRNA for KIAA49 gene; partial cds | TM |
| 192 | 11027 | 2,1 | AA161292 | INTERFERON-ALPHA INDUCIBLE 115 KD PROTEIN | other |
| 193 | 11116 | 2,1 | AA236972 | ESTs; Moderately similar to III ALU SUBFAMILY J WARNING ENTRY (III) | other |
| 194 | 11840 | 2,1 | AA300665 | ESTs; Weakly similar to Similarity to Yeast hypothetical protein YOR3140 | other |
| 195 | 11937 | 2,1 | AA111889 | segment epithelium-derived factor | other |
| 196 | 13286 | 2,1 | H18947 | ESTs | other |
| 197 | 20122 | 2,1 | N26259 | ESTs; Weakly similar to uroporphomogen III synthase, URQIIIS [H.sapien] | other |
| 198 | 20345 | 2,1 | N91492 | Human sapiens clone c28 unknown mRNA, complete sequence | other |
| 199 | 20997 | 2,1 | N8464 | ESTs | other |
| 200 | 27108 | 2,1 | AA112452 | ESTs | other |
| 201 | 28038 | 2,1 | AA488433 | ESTs; Weakly similar to deduced amino acid sequence is highly homologous | other |
| 202 | 28167 | 2,1 | AA521256 | ESTs; Highly similar to nuclear pore complex protein NUP17 [R. norvegicus] | other |
| 203 | 28358 | 2,1 | AA621604 | ESTs | other |
| 204 | 28719 | 2,1 | D59570 | ESTs | other |
| 205 | 28885 | 2,1 | P04674 | Human sapiens mRNA for KIAA146 protein; partial cds | other |
| 206 | 32124 | 2,1 | R40665 | eukaryotic translation initiation factor 3, subunit 7 (e3h7, S67K0) | other |
| 207 | 33133 | 2,1 | V00653 | ESTs; Highly similar to (Gdlinn rat era.30a +145224) [H.sapiens] | other |
| 208 | 33634 | 2,1 | V06151 | ESTs; Moderately similar to ganglioside-induced differentiation associated | other |
| 209 | 35774 | 2,1 | AA112270 | ESTs; Moderately similar to ganglioside-induced differentiation associated | other |
| 210 | 35858 | 2,1 | AA4694751 | Cellulogen B | other |
| 211 | 33301 | 2,1 | D51317 | Human transcriptional coactivator PCA mRNA, complete cds | SS |
| 212 | 33645 | 2,1 | H72464 | ESTs; Weakly similar to similar to Yeast hypothetical protein L6157.12 like | SS, TM |
| 213 | 33677 | 2,1 | H78323 | Human sapiens E2F-related transcription factor (DP-1) mRNA, complete cds | other |
| 214 | 40378 | 2,1 | N27198 | ESTs | other |
| 215 | 41795 | 2,1 | T28799 | ESTs; Highly similar to TYROSINE PROTEIN KINASE RECEPTOR EPH- | TM |
| 216 | 1714 | 2 | L09804 | proteoglycan protein 2 (polonic epithelium-enriched) | TM |
| 217 | 2601 | 2 | L33300 | "Human sapiens CD21 signal transducer mRNA, complete cds and 3' region | TM |
| 218 | 3278 | 2 | M94556 | single-stranded DNA-binding protein | other |
| 219 | 4145 | 2 | U28749 | high-mobility group (nonhistone chromosomal) protein isoform 1C | TM |
| 220 | 8149 | 2 | AA364267 | ESTs; Highly similar to HYPOTHETICAL 63.7 KD PROTEIN ZK157.1 IN C | other |

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FIGURE 10 (CONT)

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| A | | B | C | D | E |
|-----|-------|-----|-------------|--|--------|
| 221 | 9844 | 2 | N33807 | ESTs; Highly similar to NED-4 PROTEIN (Homo sapiens) | other |
| 222 | 14032 | 2 | A4186092 | ESTs; Weakly similar to CH-TOG PROTEIN (H. sapiens) | TM |
| 223 | 16395 | 2 | A025673 | ESTs; Moderately similar to (define not available 418378) (H. sapiens) | TM |
| 224 | 17327 | 2 | AA112540 | ESTs | TM |
| 225 | 23083 | 2 | T30851 | abafulin conjugating enzyme EZE 1 (homologous to yeast UBC4.5) | other |
| 226 | 25625 | 2 | AA133669 | ESTs; Weakly similar to neuronal thread protein AD7c-ATP (H. sapiens) | other |
| 227 | 26073 | 2 | AA48464 | ESTs | other |
| 228 | 28700 | 2 | D51139 | ribosomal protein S28 | other |
| 229 | 29095 | 2 | R57053 | collagen-binding protein 2 (collagen 2) | other |
| 230 | 32191 | 2 | R57053 | calnexin | SS, TM |
| 231 | 32897 | 2 | YH4664 | 5' nucleotidase (CD73) | other |
| 232 | 10762 | 1,6 | A074880 | ESTs; Weakly similar to HYPOTHETICAL 85_KD PROTEIN IN CP42/ATP | other |
| 233 | 27795 | 1,6 | AA48464 | ESTs; Weakly similar to KIAA512 protein (H. sapiens) | other |
| 234 | 28700 | 1,6 | D47286 | human mRNA for KIAA555 gene; complete cds | other |
| 235 | 38144 | 1,6 | AA430186 | ESTs | TM |
| 236 | 3879 | 1,5 | AA430186 | ESTs; Weakly similar to F5A112.9 (C. elegans) | other |
| 237 | 9897 | 1,5 | R35207 | ESTs; Weakly similar to KIAA519 (H. sapiens) | other |
| 238 | 10666 | 1,5 | A037290 | ESTs | TM |
| 239 | 14977 | 1,5 | U37546 | spoonhead inhibitor 1 | other |
| 240 | 27505 | 1,5 | AA10294 | human mRNA for KIAA336 gene; complete cds | TM |
| 241 | 28278 | 1,5 | H72948 | polyoma | SS |
| 242 | 31917 | 1,5 | N98238 | ESTs | other |
| 243 | 38272 | 1,5 | AA186533 | ESTs | other |
| 244 | 41366 | 1,5 | R55342 | CD68 antigen | other |
| 245 | 41966 | 1,5 | 167710 | ESTs | ? |
| 246 | 8439 | 1,4 | AA438304 | Homo sapiens androgen receptor associated protein 24 (AR24) mRNA, c | other |
| 247 | 10311 | 1,4 | A001836 | ESTs | other |
| 248 | 10859 | 1,4 | AA112149 | ESTs | other |
| 249 | 11279 | 1,4 | AA213410 | ESTs | SS |
| 250 | 13548 | 1,4 | AA456033 | ESTs; Highly similar to HYPOTHETICAL 1.4_KD PROTEIN IN UBPS-SPT | other |
| 251 | 14340 | 1,4 | AA396653 | Homo sapiens TCFL5 mRNA for transcription factor-lta 5; complete cds | other |
| 252 | 15531 | 1,4 | R63727 | ESTs | other |
| 253 | 32180 | 1,4 | AA398722 | ESTs | other |
| 254 | 33197 | 1,4 | AA453483 | ESTs | other |
| 255 | 3344 | 1,3 | HE437152607 | Oncogene MALL, Fusion Activator | TM |
| 256 | 16272 | 1,3 | AA108232 | RENTAL TYPE 1 CTOSCELLULAR GD | other |
| 257 | 24627 | 1,3 | AA018932 | gene with multiple splice variants near HD locus on 4p16.3 | SS, TM |
| 258 | 25718 | 1,3 | AA018932 | ESTs; Highly similar to POL. POLYPROTEIN (Spizax sarcosa virus) | other |
| 259 | 33459 | 1,3 | W93403 | ESTs | other |
| 260 | 35274 | 1,3 | AA134454 | ESTs; Weakly similar to ccf, hypothetical protein [E. coli] | SS |
| 261 | 36574 | 1,3 | AA134454 | insulin-like growth factor 2 (somatomedin A) | other |
| 262 | 41546 | 1,3 | R82346 | ESTs | TM |
| 263 | 2346 | 1,2 | M17853 | lethal giant larvae (Drosophila) homolog 1 | other |
| 264 | 6383 | 1,2 | X66371 | | other |

FIGURE 10 (CONT)
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| A | B | C | D | E |
|-----|-------|---------------|--|-------|
| 265 | 2427 | Z33208 | ESTs | other |
| 266 | 27089 | AA411473 | adducin 1 (alpha) | other |
| 267 | 33177 | W73195 | ESTs | other |
| 268 | 34852 | AA347091 | ESTs | ? |
| 269 | 35225 | AA400273 | ESTs | other |
| 270 | 38479 | AA435668 | ESTs, Weakly similar to putative p15 [H sapiens] | other |
| 271 | 38477 | AA436839 | ESTs | other |
| 272 | 40975 | AA437471 | ESTs | other |
| 273 | 41874 | TS1150 | ESTs | other |
| 274 | 8235 | AA401017 | Homo sapiens mRNA for anaplastic carcinoma, cds | other |
| 275 | 9712 | M41369 | SERUM AMYLOID A-1 PROTEIN PRECURSOR | SS |
| 276 | 14758 | S41198 | H sapiens DNA for cyp related pseudogene | other |
| 277 | 15631 | X90579 | H sapiens DNA for cyp related pseudogene | other |
| 278 | 20666 | N62789 | ESTs | TM |
| 279 | 24891 | AA044502 | cerebroside (3'-phosphatidyl) sulfate galactosylceramide 3' autoradiol | TM |
| 280 | 29045 | H13649 | ESTs | other |
| 281 | 31594 | N74690 | ESTs | TM |
| 282 | 31640 | N78784 | Homo sapiens BmiL, mRNA, complete cds | other |
| 283 | 35293 | AA400013 | EST | other |
| 284 | 37583 | AA461499 | ESTs | other |
| 285 | 37682 | AA479896 | ESTs | other |
| 286 | 38397 | AA521342 | ESTs | other |
| 287 | 38652 | AA090918 | ESTs | other |
| 288 | 40397 | N29983 | ESTs, Moderately similar to III ALU CLASS C WARNING ENTRY III [H sa | other |
| 289 | 40486 | N40559 | ESTs, Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT | other |
| 290 | 41331 | R41772 | EST | other |
| 291 | 41331 | R41772 | EST | other |
| 292 | 3365 | R43590 | Homo sapiens plasminogen-like protein (PLG) mRNA, complete cds | other |
| 293 | 5742 | X53474 | ESTs | ? |
| 294 | 6007 | X63683 | SERINE/THREONINE PROTEIN KINASE NOTARE-1 | other |
| 295 | 15233 | W04960 | ESTs | other |
| 296 | 15262 | W17304 | Homo sapiens mRNA for KIAA37 protein, complete cds | other |
| 297 | 15363 | V68847 | ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN NS | other |
| 298 | 15606 | V68725 | mitogen-activated protein kinase-activated protein kinase 2 | TM |
| 299 | 18435 | AA233989 | ESTs | other |
| 300 | 21786 | R41999 | ESTs | TM |
| 301 | 25306 | AA065081 | zml134.3.1 Strigolactone paucicreas (p33726) Homo sapiens cDNA clone IMA | other |
| 302 | 29111 | H40486 | ESTs, Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H sa | other |
| 303 | 34743 | AA302772 | ESTs, Weakly similar to neuronal thread protein ADTC-NTP [H sapiens] | other |
| 304 | 34801 | AA342526 | ESTs, Moderately similar to unknown [H sapiens] | other |
| 305 | 35355 | AA400521 | ESTs | other |
| 306 | 35940 | AA446649 | ESTs | other |
| 307 | 39221 | C71330 | ESTs | other |
| 308 | 1322 | HG4535-HF4940 | Demain | other |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------------|-----------------------|---|------------------------|
| 134804 | 12.3 | L37036 | small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78) | TM |
| 130617 | 11.4 | M90516 | glutamine-fructose-6-phosphate transaminase 1 | TM |
| 104209 | 10.6 | AB000221 | small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated | SS |
| 109991 | 10 | H09813 | ESTs | TM |
| 124315 | 8.3 | H94892 | v-rat simian leukemia viral oncogene homolog A (ras related) | Other |
| 132977 | 8.2 | U28686 | RNA binding motif protein 3 | Other |
| 130407 | 7.4 | N29888 | ESTs | Other |
| 116176 | 6.6 | AA463725 | ESTs; Weakly similar to KIAA0226 [H.sapiens] | Other |
| 119271 | 6.5 | T16387 | ESTs | Other |
| 134711 | 6.5 | X04011 | cytochrome b-245; beta polypeptide (chronic granulomatous disease) | TM |
| 134326 | 6.1 | U16306 | "Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds" | Other |
| 125852 | 5.9 | H02990 | ESTs; Weakly similar to unknown [H.sapiens] | SS, TM |
| 112169 | 5.9 | R48589 | ESTs | TM |
| 132528 | 5.9 | AA283006 | chromosome-associated polypeptide C | Other |
| 134367 | 5.7 | X54199 | phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminoimidazole synthetase | Other |
| 111929 | 5.2 | R40057 | prominin (mouse)-like 1 | SS, TM |
| 102165 | 5 | U18321 | Death associated protein 3 | Other |
| 130441 | 5 | U35835 | protein kinase; DNA-activated; catalytic polypeptide | Other |
| 133282 | 5 | U52960 | SRB7 (suppressor of RNA polymerase B; yeast) homolog | Other |
| 100783 | 4.9 | HG3748-HT4 018 | "Basic Transcription Factor, 44 Kda Subunit" | Other |
| 122223 | 4.9 | AA436158 | ESTs | Other |
| 104690 | 4.8 | AA007160 | ESTs | SS |
| 113702 | 4.8 | T97307 | ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] | Other |
| 101185 | 4.7 | L19872 | aryl hydrocarbon receptor | Other |
| 105308 | 4.7 | AA233744 | ESTs | Other |
| 107168 | 4.7 | AA621540 | ESTs | Other |
| 101201 | 4.6 | L22524 | matrix metalloproteinase 7 (matrilysin; uterine) | SS |
| 101809 | 4.5 | M86849 | "Homo sapiens connexin 26 (GJB2) mRNA, complete cds" | TM |
| 101478 | 4.5 | M23379 | RAS p21 protein activator (GTPase activating protein) 1 | Other |
| 104695 | 4.5 | AA012953 | ESTs | Other |
| 100365 | 4.4 | D78611 | mesoderm specific transcript (mouse) homolog | TM |
| 126819 | 4.3 | AA305536 | "EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence." | Other |
| 101880 | 4.3 | M97925 | defensin; alpha 5; Paneth cell-specific | SS |
| 126838 | 4.2 | AA858097 | pigment epithelium-derived factor | Other |
| 101684 | 4.2 | M63256 | cerebellar degeneration-related protein (62KD) | Other |
| 117634 | 4.2 | N35421 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | Other |
| 132109 | 4.1 | AA598801 | ESTs | Other |
| 115054 | 4.1 | AA252863 | ESTs | Other |
| 106553 | 4 | AA454967 | ESTs | Other |
| 119717 | 3.9 | W69134 | ESTs | Other |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|--|---------------------|
| 131945 | 3.9 | M87339 | replication factor C (activator 1) 4 (37kD) | Other |
| 128790 | 3.9 | AA291725 | secreted frizzled-related protein 4 | SS |
| 120562 | 3.8 | AA280038 | ESTs; Weakly similar to W01A6.c [C.elegans] | SS |
| 109517 | 3.7 | D60799 | ESTs | Other |
| 102618 | 3.7 | U85932 | extracellular matrix protein 1 | SS |
| 106286 | 3.7 | AA434441 | frizzled (Drosophila) homolog 7 | Other |
| 133640 | 3.6 | D83004 | ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) | Other |
| 100335 | 3.6 | D63391 | platelet-activating factor acetylhydrolase; isoform 1b, gamma subunit (29kD) | Other |
| 104720 | 3.6 | AA018441 | ESTs | Other |
| 107348 | 3.6 | U43701 | ribosomal protein L23a | Other |
| 134989 | 3.6 | AA236324 | ESTs; Weakly similar to !!!! ALU CLASS A WARNING ENTRY !!!! [H.sapiens] | SS |
| 111345 | 3.6 | N89820 | ESTs | Other |
| 107053 | 3.6 | AA600147 | ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans] | Other |
| 107240 | 3.5 | D59368 | ESTs | Other |
| 107129 | 3.5 | AA620553 | flap structure-specific endonuclease 1 | Other |
| 134846 | 3.5 | AA431505 | Homo sapiens mRNA for putative Sqv-7-like protein; partial | TM |
| 101897 | 3.5 | S85544 | sperm associated antigen 1 | Other |
| 107151 | 3.5 | AA621169 | ESTs | Other |
| 106012 | 3.4 | AA411621 | ESTs | Other |
| 101950 | 3.4 | S79219 | propionyl Coenzyme A carboxylase; alpha polypeptide | Other |
| 116844 | 3.4 | H84938 | ESTs | Other |
| 128025 | 3.4 | AA937173 | ESTs | TM |
| 106785 | 3.4 | AA478587 | leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL) | Other |
| 104518 | 3.4 | R09815 | proteasome (prosome; macropain) 26S subunit; ATPase; 5 | Other |
| 117667 | 3.4 | N39214 | ser-Thr protein kinase related to the myotonic dystrophy protein kinase | Other |
| 104954 | 3.3 | AA074514 | ESTs; Moderately similar to (define not available 4753768) [H.sapiens] | Other |
| 105372 | 3.3 | AA236481 | ESTs | Other |
| 104896 | 3.3 | AA054228 | ESTs | Other |
| 113485 | 3.3 | T87863 | ESTs | Other |
| 127003 | 3.3 | AA550806 | ESTs; Weakly similar to (define not available 3882151) [H.sapiens] | TM |
| 100305 | 3.3 | D50487 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase) | SS |
| 134722 | 3.2 | W47183 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens] | Other |
| 126801 | 3.2 | AA512902 | ESTs | SS, TM |
| 133503 | 3.2 | M33195 | Fc fragment of IgE; high affinity I; receptor for; gamma polypeptide | SS, TM |
| 132183 | 3.2 | L19183 | Human MAC30 mRNA; 3' end | TM |
| 105298 | 3.2 | AA233459 | ESTs | TM |
| 111046 | 3.2 | N55514 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens] | TM |
| 135309 | 3.2 | D25984 | ESTs | SS |
| 102808 | 3.2 | U90426 | nuclear RNA helicase; DECD variant of DEAD box family | Other |
| 100552 | 3.1 | HG2167-HT2 237 | "Protein Kinase Ht31, Camp-Dependent" | Other |
| 127652 | 3.1 | AA804487 | ESTs | Other |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|---|---------------------|
| 116127 | 3.1 | AA459703 | ESTs; Moderately similar to coded for by C. elegans cDNA CEESD64F [C.elegans] | TM |
| 131904 | 3.1 | AA143019 | ESTs; Highly similar to surface 4 integral membrane protein [H.sapiens] | TM |
| 126547 | 3.1 | U47732 | transmembrane 4 superfamily member 3 | Other |
| 102823 | 3.1 | U90914 | carboxypeptidase D | SS |
| 132298 | 3.1 | N41849 | Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds | Other |
| 127445 | 3.1 | AA906266 | ESTs | Other |
| 134395 | 3.1 | L09717 | lysosomal-associated membrane protein 2 | SS, TM |
| 105743 | 3.1 | AA293300 | ESTs; Weakly similar to semaphorin C [M.musculus] | Other |
| 125627 | 3.1 | AI471525 | YY1 transcription factor | Other |
| 101229 | 3.1 | L27943 | cytidine deaminase | Other |
| 102306 | 3 | U33317 | -defensin; alpha 6; Paneth cell-specific | SS |
| 107318 | 3 | T74445 | "yc82B.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence" | Other |
| 120983 | 3 | AA398209 | EST | Other |
| 134700 | 3 | AA481414 | golgi SNAP receptor complex member 1 | TM |
| 131216 | 3 | D31058 | ESTs | SS |
| 127565 | 3 | D79516 | "HUM272B04B Human aorta polyA+ (TFujiwara) Homo sapiens cDNA done GEN:272B04 5', mRNA sequence." | Other |
| 106682 | 2.9 | AA489009 | ESTs | Other |
| 130874 | 2.9 | T08287 | ESTs | Other |
| 101275 | 2.9 | L37936 | Ts translation elongation factor; mitochondrial | Other |
| 111179 | 2.9 | N67239 | ESTs | Other |
| 126086 | 2.9 | H70975 | "y73g01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence." | Other |
| 105365 | 2.9 | AA236275 | ESTs | Other |
| 118769 | 2.9 | N75416 | ESTs | Other |
| 115117 | 2.9 | AA256482 | H.sapiens PAP mRNA | Other |
| 100484 | 2.9 | HG1103-HT1 103 | "Guanine Nucleotide-Binding Protein Ras, Ras-Oncogene Related" | Other |
| 101300 | 2.9 | L40391 | Homo sapiens (clone s153) mRNA fragment | Other |
| 103075 | 2.9 | X59543 | ribonucleotide reductase M1 polypeptide | Other |
| 132164 | 2.8 | U84573 | procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 | Other |
| 106716 | 2.8 | AA464962 | ESTs | Other |
| 134098 | 2.8 | X06323 | Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3 | Other |
| 134485 | 2.8 | X82153 | cathpsin K (pseudocystosis) | SS |
| 129634 | 2.8 | AA150726 | ESTs | Other |
| 112207 | 2.8 | R49602 | ESTs | Other |
| 124904 | 2.8 | R86970 | ESTs | Other |
| 125471 | 2.8 | AA477571 | UDP-glucose ceramide glucosyltransferase | SS |
| 132180 | 2.8 | AA405569 | fibroblast activation protein; alpha | SS |
| 104454 | 2.8 | M84443 | galactokinase 2 | TM |
| 134282 | 2.8 | T25508 | ESTs | Other |
| 101558 | 2.8 | M32011 | neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease; autosomal 2) | Other |
| 130529 | 2.8 | AA173238 | small inducible cytokine A5 (RANTES) | Other |
| 101804 | 2.7 | M86699 | TTK protein kinase | Other |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|--|---------------------|
| 108565 | 2.7 | F01930 | ESTs | Other |
| 112427 | 2.7 | R62604 | ESTs | Other |
| 115188 | 2.7 | AA251819 | ESTs | Other |
| 121831 | 2.7 | AA425374 | ESTs | Other |
| 132454 | 2.7 | W78726 | ESTs; Highly similar to serine/threonine kinase [H.sapiens] | Other |
| 116399 | 2.7 | AA599729 | Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds | Other |
| 100409 | 2.7 | D86957 | Human mRNA for KIAA0202 gene; partial cds | Other |
| 130987 | 2.7 | R45698 | ESTs | Other |
| 107217 | 2.7 | D51095 | ESTs | SS, TM |
| 125698 | 2.6 | AA748483 | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes; complete cds | SS |
| 118722 | 2.6 | N73563 | ESTs | SS |
| 104521 | 2.6 | R11604 | "Y47c1.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:132 5', mRNA sequence" | Other |
| 130800 | 2.6 | AA223386 | ESTs; Weakly similar to katanin p80 subunit [H.sapiens] | Other |
| 134415 | 2.6 | AA329274 | protein tyrosine phosphatase type IVA; member 2 | TM |
| 116461 | 2.6 | AA621557 | ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens] | Other |
| 100894 | 2.6 | HG4297-HT4 567 | Transcriptional Coactivator Pca4 | Other |
| 103818 | 2.6 | AA150614 | "z143n5.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5', mRNA sequence" | Other |
| 105713 | 2.6 | AA291321 | ESTs | Other |
| 114959 | 2.6 | AA250775 | ESTs | Other |
| 130415 | 2.6 | X07290 | Human HF_12 gene mRNA | Other |
| 101791 | 2.6 | M83822 | Human beige-like protein (BGL) mRNA; partial cds | Other |
| 128131 | 2.6 | A1283162 | claudin 3 | SS, TM |
| 131584 | 2.6 | AA461465 | ESTs | Other |
| 100279 | 2.6 | D42084 | Human mRNA for KIAA0094 gene; partial cds | Other |
| 130149 | 2.6 | J04031 | methyleneletrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase, formyletrahydrofolate synthetase | Other |
| 118988 | 2.6 | W61710 | ESTs | SS |
| 126638 | 2.6 | AA649257 | ESTs | Other |
| 131672 | 2.6 | X12901 | Human mRNA for villin | Other |
| 134405 | 2.6 | J04177 | collagen; type XI; alpha 1 | Other |
| 101188 | 2.5 | L20320 | cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase) | TM |
| 104534 | 2.5 | R22303 | ESTs; Weakly similar to putative p150 [H.sapiens] | Other |
| 135179 | 2.5 | U43747 | Friedreich ataxia | SS |
| 124308 | 2.5 | H93575 | ESTs | SS |
| 125621 | 2.5 | A1051602 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase) | TM |
| 101342 | 2.5 | L76191 | interleukin-1 receptor-associated kinase 1 | Other |
| 129351 | 2.5 | AA167268 | ESTs | Other |
| 103774 | 2.5 | AA028938 | ESTs; Weakly similar to ROTG3.8 [C.elegans] | Other |
| 131289 | 2.5 | AA485697 | ESTs | SS, TM |
| 132094 | 2.5 | W01996 | ESTs; Highly similar to (define not available 4929653) [H.sapiens] | Other |
| 103223 | 2.5 | X74801 | chaperonin containing TCP1; subunit 3 (gamma) | Other |

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FIGURE 11 (CONT)

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|--|---------------------|
| 105610 | 2.5 | AA279991 | ESTs | Other |
| 115719 | 2.5 | AA416997 | ESTs | Other |
| 134888 | 2.5 | AA148094 | Tat-interacting protein (30kD) | Other |
| 105564 | 2.5 | AA262943 | ESTs | Other |
| 129689 | 2.5 | AA130156 | ESTs | Other |
| 103391 | 2.5 | X94453 | pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) | Other |
| 104182 | 2.5 | AA479990 | ESTs; Weakly similar to glioma amplified on chromosome 1 protein [H.sapiens] | SS, TM |
| 123494 | 2.5 | AA599786 | ESTs | Other |
| 122905 | 2.5 | AA470070 | ESTs | Other |
| 109175 | 2.5 | AA180496 | ESTs | Other |
| 129907 | 2.5 | D80170 | ESTs | Other |
| 115142 | 2.4 | AA258116 | ESTs; Weakly similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens] | Other |
| 125474 | 2.4 | AA151216 | Homo sapiens 14-3-3 protein mRNA; complete cds | SS |
| 125745 | 2.4 | A1283493 | ribophorin II | Other |
| 100103 | 2.4 | AF007875 | dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit | Other |
| 102687 | 2.4 | U73379 | Human cyclin-selective ubiquitin carrier protein mRNA; complete cds | Other |
| 133170 | 2.4 | U21049 | epithelial protein up-regulated in carcinoma | SS, TM |
| 109141 | 2.4 | AA176428 | ESTs | Other |
| 132811 | 2.4 | U25435 | transcriptional repressor | Other |
| 102862 | 2.4 | X01057 | interleukin 2 receptor; alpha | SS, TM |
| 104300 | 2.4 | D37933 | synixin 1B | Other |
| 105091 | 2.4 | AA148859 | ESTs; Moderately similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens] | Other |
| 110674 | 2.4 | H89315 | gamma25e05.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence. | TM |
| 122571 | 2.4 | AA452600 | EST | Other |
| 123421 | 2.4 | AA568440 | ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens] | Other |
| 132181 | 2.4 | AA046639 | !!!! [H.sapiens] | Other |
| 129445 | 2.4 | AA306121 | ESTs | SS |
| 113923 | 2.4 | W80703 | ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus] | Other |
| 100598 | 2.4 | HG2463-HT2 559 | Guanine Nucleotide-Binding Protein G25k | Other |
| 130669 | 2.4 | AA128100 | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) | Other |
| 132393 | 2.4 | W85686 | ESTs; Moderately similar to !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! [H.sapiens] | Other |
| 100630 | 2.4 | HG4074-HT4 344 | Rad2 | Other |
| 133765 | 2.4 | D21255 | cacherin 11 (OB-cacherin; osteoblast) | SS, TM |
| 100867 | 2.4 | HG4316-HT4 586 | Transketolase-Like Protein | Other |
| 119859 | 2.4 | W80702 | ESTs | Other |
| 135269 | 2.4 | M77698 | YY1 transcription factor | Other |
| 115140 | 2.4 | AA258030 | ESTs; Weakly similar to (define not available 3874621) [C.elegans] | Other |
| 102162 | 2.4 | U19291 | CDC16 (cell division cycle 16; S. cerevisiae; homolog) | Other |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|---|---------------------|
| 100372 | 2.4 | D79997 | KIAA0175 gene product | TM |
| 106981 | 2.4 | AA521157 | ESTs | Other |
| 130114 | 2.4 | AA234717 | ESTs | Other |
| 116129 | 2.3 | AA459956 | ESTs | Other |
| 122235 | 2.3 | AA436475 | ESTs | Other |
| 107315 | 2.3 | T62771 | Homo sapiens nucleoplasmin-3 (NPM3) mRNA: complete cds | SS |
| 125905 | 2.3 | T69868 | chaperonin containing TCP1; subunit 2 (beta) | Other |
| 133061 | 2.3 | AB000594 | prostate differentiation factor | SS |
| 107531 | 2.3 | Y13636 | protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform | Other |
| 125820 | 2.3 | AA730136 | teratocarcinoma-derived growth factor 1 | Other |
| 131725 | 2.3 | AA456264 | ESTs; Highly similar to (define not available 4175448) [H.sapiens] | Other |
| 101228 | 2.3 | T27706 | chaperonin containing TCP1; subunit 6A (zebra 1) | Other |
| 132571 | 2.3 | R84594 | ESTs; Highly similar to (define not available 4809026) [H.sapiens] | SS, TM |
| 100090 | 2.3 | AC002486 | "Human BAC clone RG367O17 from 7p15-p21, complete sequence [Homo sapiens]" | Other |
| 103658 | 2.3 | Z74615 | collagen; type I; alpha 1 | SS, TM |
| 104897 | 2.3 | AA054641 | ESTs | Other |
| 106818 | 2.3 | AA480890 | ESTs | Other |
| 113077 | 2.3 | T40442 | ESTs | SS |
| 128773 | 2.3 | M28870 | granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1) | SS |
| 129506 | 2.3 | AA258286 | Homo sapiens mRNA for KIAA0877 protein; partial cds | TM |
| 133746 | 2.3 | U44378 | MAD (mothers against decapentaplegic; Drosophila) homolog 4 | Other |
| 134272 | 2.3 | X76040 | Lon protease-like protein | Other |
| 106267 | 2.3 | AA431873 | Homo sapiens clone 24711 mRNA sequence | Other |
| 133463 | 2.3 | AA284143 | Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA; complete cds | Other |
| 104278 | 2.3 | C02582 | ESTs; Highly similar to (define not available 5114045) [H.sapiens] | Other |
| 127211 | 2.3 | AA480935 | "aa28c03.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5', mRNA sequence." | Other |
| 110721 | 2.3 | H97678 | ESTs | Other |
| 114774 | 2.3 | AA150043 | ESTs | TM |
| 132968 | 2.3 | N77151 | Homo sapiens mRNA for KIAA0799 protein; partial cds | Other |
| 106916 | 2.3 | AA490814 | ESTs | Other |
| 113849 | 2.3 | W60439 | ESTs; Moderately similar to cbp146 [M.musculus] | Other |
| 131028 | 2.3 | U20240 | CCAAT/enhancer binding protein (C/EBP); gamma | Other |
| 130380 | 2.3 | U55853 | Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds | SS |
| 125390 | 2.3 | H95094 | KIAA0016 gene product | SS, TM |
| 127296 | 2.3 | AA327550 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens] | Other |
| 132116 | 2.3 | AA234767 | ESTs | SS, TM |
| 117765 | 2.3 | N47797 | ESTs | Other |
| 119126 | 2.3 | R45175 | ESTs | Other |
| 129482 | 2.2 | AA435949 | ESTs; Moderately similar to unknown protein [H.sapiens] | Other |
| 120493 | 2.2 | AA258933 | ESTs | SS |
| 108927 | 2.2 | AA143493 | ESTs; Weakly similar to PLECKSTRIN [H.sapiens] | Other |

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FIGURE 11 (CONT)

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|---|---------------------|
| 122520 | 2.2 | AA449427 | ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens] | Other |
| 125982 | 2.2 | R98091 | RAE1 (RNA export 1; S.pombe) homolog | Other |
| 132325 | 2.2 | N37055 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens] | Other |
| 100287 | 2.2 | D43950 | Human mRNA for KIAA0098 gene; partial cds | Other |
| 114895 | 2.2 | AA236177 | Homo sapiens mRNA for KIAA0087 protein; partial cds | Other |
| 105038 | 2.2 | AA130273 | ESTs; Weakly similar to (define not available 4240269) [H.sapiens] | Other |
| 105476 | 2.2 | AA255473 | ESTs | SS |
| 106942 | 2.2 | AA496347 | ESTs; Highly similar to gene 7442 protein [H.sapiens] | Other |
| 110566 | 2.2 | H59990 | ESTs | Other |
| 111068 | 2.2 | N58397 | ESTs | Other |
| 127963 | 2.2 | AI299013 | "gn13h12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1696183 3' similar to TR022813 Q22813 PUTATIVE NAD(P)-DEPENDENT CHOLESTEROL DEHYDROGENASE. ; mRNA sequence." | TM |
| 130985 | 2.2 | AA243700 | ESTs | Other |
| 132877 | 2.2 | R40685 | Homo sapiens mRNA for KIAA0851 protein; complete cds | TM |
| 135242 | 2.2 | M74093 | cyclin E1 | TM |
| 129468 | 2.2 | J03040 | secreted protein; acidic; cysteine-rich (osteonectin) | SS |
| 132616 | 2.2 | AA386264 | ESTs | SS, TM |
| 133780 | 2.2 | M14219 | desotin | Other |
| 121653 | 2.2 | AA425887 | ESTs | Other |
| 114608 | 2.2 | AA079381 | ESTs | Other |
| 129017 | 2.2 | H13106 | ESTs | SS |
| 132725 | 2.2 | L41887 | splicing factor; arginine/serine-rich 7 (35kD) | Other |
| 125606 | 2.2 | R28463 | ESTs | SS |
| 105538 | 2.2 | AA258660 | ESTs; Highly similar to (define not available 4583654) [H.sapiens] | Other |
| 133221 | 2.2 | AA235289 | ESTs; Highly similar to rap2 gene product [H.sapiens] | Other |
| 106369 | 2.2 | AA446949 | ESTs | Other |
| 128949 | 2.2 | AA190993 | a disintegrin and metalloproteinase domain 12 (meltrin alpha) | Other |
| 120959 | 2.2 | AA398116 | ESTs | Other |
| 102495 | 2.2 | U51240 | Human mRNA for KIAA0085 gene; partial cds | TM |
| 101124 | 2.2 | L10343 | protease inhibitor 3; skin-derived (SKALP) | SS |
| 102778 | 2.2 | U83463 | syndecan binding protein (syntenin) | Other |
| 107307 | 2.2 | T52099 | creatine kinase; mitochondrial 2 (sarcomeric) | Other |
| 111605 | 2.2 | R11638 | ESTs | Other |
| 101959 | 2.2 | S80343 | arginyl-tRNA synthetase | Other |
| 101031 | 2.2 | J05070 | matrix metalloproteinase 9 (gelatinase B; 92kD gelatinase; 92kD type IV collagenase) | SS |
| 131701 | 2.2 | AA149006 | ESTs; Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens] | Other |
| 105344 | 2.2 | AA235303 | ESTs | TM |
| 103166 | 2.2 | X67951 | proliferation-associated gene A (natural killer-enhancing factor A) | Other |
| 131463 | 2.2 | X74142 | forkhead (Drosophila)-like 1 | Other |
| 131412 | 2.2 | U34044 | Human selenium donor protein (selD) mRNA; complete cds | Other |
| 134982 | 2.2 | N46086 | ESTs | Other |
| 127236 | 2.1 | AJ341818 | budding uninhibited by benzimidazoles 1 (yeast homolog) | Other |
| 104459 | 2.1 | M91493 | EST | Other |

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FIGURE 11 (CONT)

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|--|---------------------|
| 124596 | 2.1 | N70088 | ESTs | Other |
| 105650 | 2.1 | AA282347 | ESTs; Highly similar to (define not available 4454694) [H.sapiens] | Other |
| 134917 | 2.1 | X87241 | FAT tumor suppressor (Drosophila) homolog | SS |
| 132478 | 2.1 | H20906 | Homo sapiens mRNA for KIAA0746 protein; partial cds | SS, TM |
| 134464 | 2.1 | N79354 | ESTs; Weakly similar to Rga [D.melanogaster] | Other |
| 111221 | 2.1 | N68869 | ESTs | Other |
| 100892 | 2.1 | HG4557-HT4 | | |
| 100892 | 2.1 | 962 | "Small Nuclear Ribonucleoprotein U1, 1snrp" | Other |
| 117170 | 2.1 | H98153 | ESTs | Other |
| 124049 | 2.1 | F10523 | primase; polypeptide 2A (58kD) | Other |
| 131892 | 2.1 | D50914 | Human mRNA for KIAA0124 gene; partial cds | TM |
| 103003 | 2.1 | X52003 | trefoil factor 1 (breast cancer; estrogen-inducible sequence expressed in) | SS |
| 134085 | 2.1 | U20979 | chromatin assembly factor I (150 kDa) | Other |
| 126216 | 2.1 | N23870 | ESTs | Other |
| 102721 | 2.1 | U79241 | Human clone 23759 mRNA; partial cds | Other |
| 128040 | 2.1 | AA918528 | ESTs | Other |
| 101038 | 2.1 | J05249 | replication protein A2 (32kD) | SS |
| 106060 | 2.1 | AA417287 | C-terminal binding protein 2 | Other |
| 103622 | 2.1 | Z49042 | basic transcription factor 3 | Other |
| 127884 | 2.1 | AA758630 | ESTs | Other |
| 130911 | 2.1 | W72906 | HIRA interacting protein 4 (dnaJ-like) | Other |
| 104260 | 2.1 | AF008192 | Homo sapiens putative GR6 protein (GR6) mRNA; complete cds | Other |
| 120714 | 2.1 | AA292689 | ESTs | Other |
| 101578 | 2.1 | M34423 | galactosidase; beta 1 | SS |
| 113443 | 2.1 | T86158 | ESTs | SS |
| 101516 | 2.1 | M28249 | Accession not listed in Genbank | Other |
| 106480 | 2.1 | AA450373 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY | Other |
| 111365 | 2.1 | N92659 | ESTs | Other |
| 121121 | 2.1 | AA399371 | ESTs; Weakly similar to (define not available 4688925) [H.sapiens] | Other |
| 124768 | 2.1 | R40177 | ESTs | Other |
| 102501 | 2.1 | U51586 | Human slah binding protein 1 (SlahBP1) mRNA; partial cds | Other |
| 106432 | 2.1 | AA448850 | ESTs | Other |
| 132812 | 2.1 | R48108 | ESTs | Other |
| 125681 | 2.1 | AA394176 | accessory proteins BAP31/BAP29 | TM |
| 130511 | 2.1 | L32137 | cartilage oligomeric matrix protein | Other |
| 128219 | 2.1 | AA978333 | ESTs | Other |
| 130962 | 2.1 | AA102051 | transmembrane 4 superfamily member 6 | SS, TM |
| 101840 | 2.1 | M93056 | protease inhibitor 2 (anti-elastase); monocyte/neutrophil | TM |
| 123928 | 2.1 | AA621363 | EST | Other |
| 132073 | 2.1 | N67408 | ESTs; Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY | Other |
| 101671 | 2.1 | M61832 | !!!! [H.sapiens] | Other |
| 107059 | 2.1 | AA608545 | S-adenosylhomocysteine hydrolase | Other |
| 132791 | 2.1 | AA446088 | ESTs | Other |
| 103131 | 2.1 | X85614 | ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens] | Other |
| 104791 | 2.1 | AA029046 | S100 calcium-binding protein P | Other |
| 104791 | 2.1 | AA029046 | ESTs | Other |

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FIGURE 11 (CONT)

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------|--------------------|---|---------------------|
| 138181 | 2.1 | AA621349 | ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans] | Other |
| 104334 | 2.1 | D82614 | ESTs | Other |
| 132103 | 2.1 | AA025086 | ESTs | Other |
| 126743 | 2.1 | AA179253 | poly(A)-binding protein-like 1 | Other |
| 100439 | 2.1 | D87453 | Human mRNA for KIAA0264 gene; partial cds | Other |
| 114860 | 2.1 | AA235112 | ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens] | Other |
| 116732 | 2.1 | F13779 | ESTs; Weakly similar to [!!!] ALU SUBFAMILY J WARNING ENTRY [!!!] [H.sapiens] | Other |
| 131045 | 2.1 | H30863 | ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens] | Other |
| 133209 | 2.1 | AA114163 | ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens] | Other |
| 101758 | 2.1 | M77836 | Human pyrroline 5-carboxylate reductase mRNA; complete cds | Other |
| 102214 | 2.1 | U23752 | SRV (sex-determining region Y)-box 11 | Other |
| 130100 | 2.1 | AA425593 | ESTs | Other |
| 109799 | 2.1 | F10770 | Homo sapiens clone 669 unknown mRNA; complete sequence | Other |
| 130860 | 2.1 | U86061 | T-cell receptor; beta cluster | SS, TM |
| 106885 | 2.1 | AA461551 | ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens] | TM |
| 125724 | 2.1 | AA083407 | stimulated trans-acting factor (50 kDa) | Other |
| 134258 | 2.1 | L28010 | heterogeneous nuclear ribonucleoprotein F | Other |
| 129642 | 2.1 | R50008 | 7-dehydrocholesterol reductase | TM |
| 125336 | 2.1 | T86823 | ESTs | Other |
| 125303 | 2 | Z39821 | ESTs | Other |
| 100749 | 2 | HG3521-HT3 715 | Ras-Related Protein Rap1b | Other |
| 126185 | 2 | AI393989 | ESTs | TM |
| 126880 | 2 | AI151406 | ESTs | SS, TM |
| 105263 | 2 | AA227926 | ESTs | Other |
| 123288 | 2 | AA495836 | EST | Other |
| 105807 | 2 | AA393803 | ESTs | Other |
| 105040 | 2 | AA131047 | KIAA0698 gene product | TM |
| 131977 | 2 | F09788 | procollagen-proline; 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide II | SS |
| 117982 | 2 | N52000 | ESTs | SS, TM |
| 134037 | 2 | X53586 | Human mRNA for integrin alpha 8 | SS |
| 132744 | 2 | X54326 | glutaryl-prolyl-HRNA synthetase | Other |
| 101581 | 2 | M34995 | "Human MHC cell surface glycoprotein (HLA-DOA) mRNA, 3'end" | SS, TM |
| 103576 | 2 | Z26317 | desmoglein 2 | SS |
| 131235 | 2 | AA223284 | ESTs; Moderately similar to (define not available 4680395) [H.sapiens] | Other |
| 127910 | 2 | AA781881 | ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus] | SS |
| 101552 | 2 | M31042 | hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) | Other |
| 106318 | 2 | AA436570 | Homo sapiens mRNA for pre-mRNA cleavage factor I subunit | Other |
| 101192 | 2 | L20859 | Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds | TM |
| 104592 | 2 | R81003 | Homo sapiens serine protease mRNA; complete cds | SS |
| 129095 | 2 | L12350 | thrombospondin 2 | SS |

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| PRIMEKEY | Fold Upregulated in Tumors | Exemplar Accession | Complete Title | ORF Structural Info |
|----------|----------------------------------|-----------------------|--|------------------------|
| 105705 | 2 | AA290767 | ESTs | Other |
| 128461 | 2 | M63262 | arachidonate 5-lipoxygenase-activating protein | SS, TM |

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| Primary Seq | Accession | Gene Description | Feature Info |
|-------------|--------------|------------------|--------------|
| 16074 | >10 AA001507 | ESTs | other |
| 25047 | >10 AA011031 | ESTs | other |
| 25082 | >10 AA017257 | ESTs | other |
| 16490 | >10 AA026418 | ESTs | other |
| 25179 | >10 AA031268 | H.sapiens miR | other |
| 25215 | >10 AA035540 | APOLipoprotein | other |
| 25282 | >10 AA044825 | ESTs | other |
| 16810 | >10 AA053636 | ESTs | other |
| 16935 | >10 AA054438 | ESTs | SS, |
| 10747 | >10 AA055841 | ESTs | other |
| 10748 | >10 AA055892 | ESTs | other |
| 16993 | >10 AA065300 | Human mRNA | other |
| 17051 | >10 AA070801 | ESTs | TM |
| 10840 | >10 AA084104 | ESTs | other |
| 7296 | >10 AA085661 | ESTs | other |
| 7325 | >10 AA090842 | ESTs Weakly | other |
| 17419 | >10 AA113349 | EST | ? |
| 17541 | >10 AA127459 | ESTs | other |
| 17559 | >10 AA128407 | ESTs | other |
| 25669 | >10 AA128978 | ESTs | ? |
| 17600 | >10 AA130596 | ESTs | other |
| 10992 | >10 AA132523 | Homo sapiens | other |
| 17654 | >10 AA133250 | ESTs | TM |
| 17734 | >10 AA137246 | ESTs | other |
| 25801 | >10 AA148530 | EST - RC, AA | TM |
| 25806 | >10 AA149007 | EST | ? |
| 11121 | >10 AA156359 | Human TAR O | ? |
| 11160 | >10 AA164269 | ESTs | other |
| 25925 | >10 AA164494 | ESTs Weakly | other |
| 25934 | >10 AA165355 | Human clone | ? |
| 17987 | >10 AA169379 | ESTs | other |
| 18008 | >10 AA171895 | Homo sapiens | TM |
| 33953 | >10 AA173290 | Human HOXA | other |
| 33990 | >10 AA180223 | CAMP-DEPENDENT | other |
| 34013 | >10 AA190688 | EST - RC, AA | other |
| 34014 | >10 AA191348 | ESTs | other |
| 34015 | >10 AA191353 | ESTs | TM |
| 34070 | >10 AA196549 | ESTs | other |
| 18260 | >10 AA206801 | ESTs | ? |
| 34105 | >10 AA207123 | ESTs | SS, |
| 34107 | >10 AA209469 | ESTs | other |
| 18330 | >10 AA216722 | Human mRNA | TM |
| 18362 | >10 AA223912 | Ribonuclease | other |
| 18392 | >10 AA227751 | ESTs | SS, |
| 34188 | >10 AA228030 | ESTs | TM |
| 34197 | >10 AA232315 | Homo sapiens | other |
| 25948 | >10 AA234365 | Homo sapiens | ? |
| 25951 | >10 AA234556 | EST | ? |
| 11561 | >10 AA236533 | Evi-1 | other |
| 26059 | >10 AA236685 | ESTs | other |
| 26100 | >10 AA242835 | Human mRNA | other |
| 11603 | >10 AA243052 | ESTs Highly | other |
| 7785 | >10 AA243375 | EST - AA2433 | other |
| 34372 | >10 AA251973 | ESTs | ? |
| 25240 | >10 AA252282 | Human mRNA | TM |

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| | | | | |
|-------|-----|----------|----------------|-------|
| 34362 | >10 | AA252512 | ESTs | other |
| 34391 | >10 | AA252703 | EST - RC_AA | other |
| 26274 | >10 | AA253011 | ESTs | ? |
| 34400 | >10 | AA253400 | ESTs | other |
| 26291 | >10 | AA253422 | ESTs | ? |
| 26355 | >10 | AA256379 | ESTs | other |
| 11813 | >10 | AA258158 | ESTs | other |
| 34518 | >10 | AA278721 | ESTs | ? |
| 28545 | >10 | AA278979 | ESTs | other |
| 26574 | >10 | AA279504 | ESTs | other |
| 34554 | >10 | AA290016 | DNA polymerase | other |
| 34561 | >10 | AA280298 | ESTs | TM |
| 26628 | >10 | AA280641 | ESTs Highly | TM |
| 11969 | >10 | AA280670 | ESTs | SS, |
| 34575 | >10 | AA280738 | ESTs | TM |
| 26677 | >10 | AA281636 | ESTs | ? |
| 26700 | >10 | AA282197 | EST | ? |
| 34672 | >10 | AA284372 | ESTs | other |
| 34692 | >10 | AA285079 | ESTs | other |
| 12143 | >10 | AA290991 | ESTs | other |
| 8092 | >10 | AA316272 | ESTs | TM |
| 34904 | >10 | AA321746 | EST | other |
| 8111 | >10 | AA323787 | ESTs | other |
| 8125 | >10 | AA330771 | Human protein | TM |
| 26916 | >10 | AA331393 | ESTs | other |
| 26926 | >10 | AA342402 | ESTs | other |
| 26935 | >10 | AA347193 | ESTs Weakly | TM |
| 35038 | >10 | AA350541 | ESTs Moderate | TM |
| 35049 | >10 | AA350857 | ESTs | other |
| 35106 | >10 | AA371561 | EST Weakly | ? |
| 35197 | >10 | AA398120 | ESTs | other |
| 35277 | >10 | AA398536 | ESTs | other |
| 35309 | >10 | AA398660 | EST | other |
| 35322 | >10 | AA398710 | H. sapiens RNA | TM |
| 27037 | >10 | AA400198 | ESTs | TM |
| 35495 | >10 | AA400527 | ESTs | ? |
| 27046 | >10 | AA400670 | Homo sapiens | other |
| 35500 | >10 | AA400715 | ESTs | other |
| 12480 | >10 | AA403116 | Homo sapiens | other |
| 35663 | >10 | AA405485 | ESTs Weakly | other |
| 35697 | >10 | AA405512 | ESTs | other |
| 35766 | >10 | AA408169 | Homo sapiens | other |
| 35769 | >10 | AA408206 | ESTs | other |
| 35798 | >10 | AA410231 | ESTs | other |
| 35801 | >10 | AA410291 | ESTs | other |
| 35803 | >10 | AA410295 | ESTs | other |
| 35822 | >10 | AA411144 | ESTs | TM |
| 35874 | >10 | AA412024 | EST | ? |
| 35956 | >10 | AA412550 | ESTs | other |
| 36052 | >10 | AA417027 | EST | TM |
| 36258 | >10 | AA423962 | ESTs Weakly | other |
| 36268 | >10 | AA424502 | ESTs | other |
| 36307 | >10 | AA424803 | EST | ? |
| 36371 | >10 | AA426017 | ESTs | TM |
| 36395 | >10 | AA426353 | ESTs | other |
| 36405 | >10 | AA426406 | Homo sapiens | other |

FIGURE 12
(cont.)

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| | | | | |
|-------|-----|----------|--------------|--------|
| 36506 | >10 | AA429610 | ESTs | other |
| 36571 | >10 | AA430726 | EST - RC_AA | SS, |
| 36695 | >10 | AA433910 | ESTs | other |
| 36739 | >10 | AA435610 | EST - RC_AA | ? |
| 36753 | >10 | AA435686 | ESTs | other |
| 36845 | >10 | AA436198 | ESTs | ? |
| 13136 | >10 | AA436560 | ESTs | SS, TM |
| 13143 | >10 | AA436619 | ESTs | SS, |
| 36958 | >10 | AA442060 | ESTs | other |
| 36962 | >10 | AA442082 | ESTs | ? |
| 36981 | >10 | AA442845 | EST | ? |
| 13237 | >10 | AA443971 | ESTs Weakly | ? |
| 13242 | >10 | AA445094 | ESTs | other |
| 37057 | >10 | AA446131 | ESTs | other |
| 37068 | >10 | AA446312 | ESTs Weakly | other |
| 37074 | >10 | AA446344 | ESTs | SS, |
| 37084 | >10 | AA446486 | Homo sapiens | ? |
| 37135 | >10 | AA447540 | EST | ? |
| 37159 | >10 | AA447714 | EST - RC_AA | other |
| 37169 | >10 | AA447772 | ESTs | ? |
| 37246 | >10 | AA449311 | Homo sapiens | other |
| 37310 | >10 | AA451707 | ESTs | other |
| 37453 | >10 | AA454610 | ESTs | ? |
| 37458 | >10 | AA454632 | ESTs | TM |
| 27787 | >10 | AA454660 | ESTs | ? |
| 37492 | >10 | AA455248 | EST - RC_AA | other |
| 37546 | >10 | AA456641 | ESTs | TM |
| 37601 | >10 | AA458864 | ESTs | other |
| 37611 | >10 | AA458996 | Human signal | SS, TM |
| 37615 | >10 | AA459101 | Human serine | other |
| 37653 | >10 | AA460017 | ESTs | other |
| 37677 | >10 | AA460530 | Homo sapiens | other |
| 37777 | >10 | AA464860 | Homo sapiens | other |
| 8648 | >10 | AA465016 | Homo sapiens | ? |
| 37816 | >10 | AA469554 | EST | ? |
| 37829 | >10 | AA470084 | ESTs | other |
| 28015 | >10 | AA477421 | ESTs | other |
| 37978 | >10 | AA479264 | EST - RC_AA | other |
| 37979 | >10 | AA479265 | ESTs Highly | other |
| 37983 | >10 | AA479348 | H.sapiens mR | other |
| 14054 | >10 | AA485223 | ESTs | TM |
| 38121 | >10 | AA485724 | EST - RC_AA | other |
| 28122 | >10 | AA485928 | ESTs Weakly | other |
| 38167 | >10 | AA487207 | EST - RC_AA | other |
| 38172 | >10 | AA487424 | EST - RC_AA | other |
| 38179 | >10 | AA487492 | Homo sapiens | other |
| 38182 | >10 | AA487501 | ESTs | other |
| 38194 | >10 | AA487959 | ESTs | other |
| 28141 | >10 | AA488432 | ESTs | ? |
| 38211 | >10 | AA488687 | ESTs | other |
| 38235 | >10 | AA489030 | ESTs | other |
| 38280 | >10 | AA489791 | EST - RC_AA | other |
| 38316 | >10 | AA490500 | Homo sapiens | other |
| 38330 | >10 | AA490882 | ESTs | other |
| 38456 | >10 | AA504343 | ESTs | SS, |
| 38460 | >10 | AA504462 | ESTs | other |

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| | | | | |
|-------|-----|---------------------|----------------|-------|
| 38553 | >10 | AA521471 | ESTs | other |
| 38580 | >10 | AA598545 | ESTs | ? |
| 38590 | >10 | AA598648 | Human mRNA | other |
| 38601 | >10 | AA598738 | ESTs | ? |
| 28323 | >10 | AA599639 | ESTs | other |
| 38828 | >10 | AA609177 | ESTs | TM |
| 38838 | >10 | AA609215 | EST - RC_AA | ? |
| 38867 | >10 | AA609318 | Human cbl-b m | TM |
| 38871 | >10 | AA609333 | EST | ? |
| 38970 | >10 | AA609749 | ESTs | other |
| 38984 | >10 | AA609839 | ESTs Modera | ? |
| 39045 | >10 | AA610077 | ESTs | other |
| 39062 | >10 | AA620333 | EST | ? |
| 39080 | >10 | AA620562 | EST - RC_AA | ? |
| 39110 | >10 | AA620709 | ESTs Weakly | other |
| 39176 | >10 | AA621091 | ESTs | other |
| 39218 | >10 | AA621330 | ESTs | other |
| 39221 | >10 | AA621346 | Homo sapiens | other |
| 39232 | >10 | AA621409 | ESTs | other |
| 21 | >10 | AB000905 | H.sapiens hist | ? |
| 8963 | >10 | AFFX-HUMTFAFFX-HUMT | | ? |
| 33890 | >10 | AFFX-HUMTFAFFX-HUMT | | ? |
| 39302 | >10 | C14944 | ESTs | other |
| 39329 | >10 | C20797 | EST | ? |
| 28644 | >10 | D12163 | ESTs | other |
| 218 | >10 | D13540 | PROTEIN-TYR | other |
| 236 | >10 | D13645 | Human mRNA | other |
| 9127 | >10 | D33037 | PHOSPHATID | other |
| 459 | >10 | D38293 | Human mRNA | TM |
| 39405 | >10 | D50975 | ESTs | other |
| 39433 | >10 | D52037 | Human thymid | other |
| 39436 | >10 | D52692 | Human Ca2+ | TM |
| 14708 | >10 | D58388 | EST | ? |
| 39488 | >10 | D60631 | ESTs | other |
| 39504 | >10 | D80632 | ESTs | other |
| 765 | >10 | D86096 | Prostaglandin | ? |
| 767 | >10 | D86969 | Human mRNA | other |
| 769 | >10 | D86971 | Human mRNA | other |
| 39529 | >10 | F02202 | ESTs | ? |
| 39535 | >10 | F02450 | ESTs Modera | TM |
| 18676 | >10 | F04022 | ESTs | other |
| 18718 | >10 | F04915 | ESTs | other |
| 18762 | >10 | F09456 | ESTs | other |
| 18782 | >10 | F09739 | ESTs | other |
| 29080 | >10 | F13655 | ESTs Modera | other |
| 19001 | >10 | H02890 | ESTs | other |
| 19164 | >10 | H10395 | EST | ? |
| 39725 | >10 | H11323 | ESTs | other |
| 19203 | >10 | H11593 | ESTs | other |
| 19328 | >10 | H17806 | ESTs | other |
| 19387 | >10 | H20128 | ESTs | ? |
| 39787 | >10 | H20131 | ESTs | SS, |
| 19389 | >10 | H20165 | EST | ? |
| 39832 | >10 | H26279 | EST - RC_H2 | other |
| 19591 | >10 | H40688 | ESTs | other |
| 29229 | >10 | H48459 | Human mRNA | other |

FIGURE 12 (cont.)

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| | | | | |
|-------|-----|------------|-----------------|--------|
| 19727 | >10 | H52702 | ESTs | ? |
| 19787 | >10 | H56679 | ESTs | other |
| 39995 | >10 | H62474 | EST | SS, TM |
| 29331 | >10 | H68116 | ESTs | TM |
| 29344 | >10 | H68839 | EST | ? |
| 40064 | >10 | H72283 | Human mRNA | other |
| 40083 | >10 | H73466 | MITOCHOND | other |
| 19949 | >10 | H76263 | ESTs | TM |
| 40204 | >10 | H88296 | EST - RC H8 | other |
| 29523 | >10 | H88353 | ESTs Weakly | ? |
| 29551 | >10 | H90134 | ESTs | ? |
| 29645 | >10 | H95640 | ESTs | ? |
| 20057 | >10 | H98079 | ESTs | other |
| 976 | >10 | HG2036-HT2 | EST - HG2036 | ? |
| 1158 | >10 | HG3344-HT3 | EST - HG3344 | ? |
| 1210 | >10 | HG37-HT37 | EST - HG37-H | ? |
| 1346 | >10 | HG4716-HT5 | EST - HG4716 | ? |
| 1349 | >10 | HG4747-HT5 | EST - HG4747 | ? |
| 1445 | >10 | J03027 | MHC class I g | ? |
| 1670 | >10 | K01383 | EST - K01383 | ? |
| 1684 | >10 | L07541 | Replication fa | other |
| 1852 | >10 | L17328 | Human FE22 | TM |
| 1856 | >10 | L18920 | MELANOMA-A | ? |
| 1863 | >10 | L19161 | TRANSLATIO | other |
| 2070 | >10 | L37378 | Homo sapiens | SS, TM |
| 2123 | >10 | L40396 | Homo sapiens | other |
| 2144 | >10 | L41349 | Phospholipase | SS, |
| 9723 | >10 | L44542 | ESTs | other |
| 2188 | >10 | L47276 | EST - L47276 | other |
| 2343 | >10 | M15353 | Eukaryotic tra | other |
| 2827 | >10 | M29610 | Glycophorin E | TM |
| 2857 | >10 | M58597 | Fucosyltransfe | TM |
| 3021 | >10 | M88941 | Protein tyrosin | other |
| 3163 | >10 | M84424 | Cathepsin E | ? |
| 3196 | >10 | M86917 | Oxysterol bind | other |
| 20088 | >10 | N20054 | ESTs Weakly | ? |
| 29795 | >10 | N20641 | ESTs Highly | other |
| 40427 | >10 | N21147 | ESTs | other |
| 40444 | >10 | N22140 | ESTs Highly | other |
| 29693 | >10 | N23003 | ESTs | TM |
| 40498 | >10 | N26086 | Homo sapiens | SS, |
| 40559 | >10 | N33024 | ESTs | SS, |
| 30190 | >10 | N33264 | EST | ? |
| 30207 | >10 | N33920 | H. sapiens mR | other |
| 20304 | >10 | N34686 | Homo sapiens | ? |
| 20307 | >10 | N34830 | ESTs | other |
| 30255 | >10 | N35115 | ESTs | other |
| 40594 | >10 | N35388 | ESTs | other |
| 40604 | >10 | N38893 | Homo sapiens | other |
| 40631 | >10 | N45124 | ESTs | other |
| 40660 | >10 | N49104 | NUCLEAR FA | other |
| 30610 | >10 | N50138 | EST | ? |
| 30617 | >10 | N50646 | ESTs | other |
| 30631 | >10 | N50807 | EST | ? |
| 30790 | >10 | N52935 | EST | ? |
| 20564 | >10 | N55443 | ESTs | TM |

FIGURE 12 (cont.)

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| | | | | |
|-------|-----|--------|----------------|-------|
| 40760 | >10 | N57927 | ESTs Weakly | other |
| 30938 | >10 | N58561 | Cathepsin B | other |
| 20614 | >10 | N59230 | ESTs | SS, |
| 20657 | >10 | N62889 | ESTs | other |
| 31136 | >10 | N63512 | ESTs Weakly | TM |
| 40827 | >10 | N64051 | Homo sapiens | other |
| 31310 | >10 | N66831 | EST | ? |
| 40876 | >10 | N67607 | Human Rho-a | other |
| 20791 | >10 | N68057 | Homo sapiens | ? |
| 40905 | >10 | N68738 | ESTs | other |
| 40911 | >10 | N69114 | H.sapiens mR | other |
| 40913 | >10 | N69218 | ESTs | other |
| 31484 | >10 | N69466 | ESTs | other |
| 31619 | >10 | N73449 | ESTs | other |
| 41005 | >10 | N79516 | ESTs | TM |
| 31818 | >10 | N89774 | Homo sapiens | other |
| 31872 | >10 | N91109 | EST | other |
| 41040 | >10 | N91948 | ESTs | other |
| 31944 | >10 | N93193 | ESTs | other |
| 41065 | >10 | N93618 | ESTs | other |
| 32034 | >10 | N98926 | ESTs Modera | other |
| 41107 | >10 | R01634 | ESTs | other |
| 41163 | >10 | R08176 | ESTs | other |
| 21238 | >10 | R08564 | Plasminogen- | other |
| 21240 | >10 | R08613 | ESTs | other |
| 21412 | >10 | R20670 | ESTs | other |
| 21519 | >10 | R27975 | EST - RC_R2 | other |
| 41381 | >10 | R42278 | H.sapiens mR | ? |
| 32189 | >10 | R43183 | ESTs | TM |
| 32195 | >10 | R43471 | ESTs Weakly | other |
| 21902 | >10 | R43622 | EST | ? |
| 21946 | >10 | R44707 | ESTs | TM |
| 22072 | >10 | R49406 | ESTs | ? |
| 32240 | >10 | R50976 | Ribonuclease | other |
| 32258 | >10 | R55623 | ESTs | other |
| 22258 | >10 | R56432 | ESTs | other |
| 22282 | >10 | R59197 | ESTs | other |
| 32277 | >10 | R61493 | Human mRNA | other |
| 22372 | >10 | R62831 | EST | ? |
| 22400 | >10 | R64109 | ESTs | other |
| 41593 | >10 | R64129 | ESTs | other |
| 10233 | >10 | R71427 | ESTs Highly | other |
| 41654 | >10 | R76437 | THROMBOXA | TM |
| 22557 | >10 | R76722 | ESTs | other |
| 22576 | >10 | R79111 | ESTs | other |
| 22593 | >10 | R79777 | EST | ? |
| 41678 | >10 | R80675 | EST | ? |
| 41719 | >10 | R89260 | EST - RC_R8 | other |
| 22793 | >10 | R96208 | ESTs | other |
| 41752 | >10 | R97063 | ESTs | other |
| 3375 | >10 | S50223 | HKR-T1 | other |
| 3406 | >10 | S66896 | SQUAMOUS | other |
| 3522 | >10 | S80267 | Spleen tyrosin | other |
| 41793 | >10 | T03887 | ESTs | ? |
| 23198 | >10 | T40530 | ESTs Weakly | other |
| 23360 | >10 | T58531 | ESTs | other |

FIGURE 12 (cont.)

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| | | | | |
|-------|-----|--------|-----------------|--------|
| 32535 | >10 | T81116 | ESTs | other |
| 42177 | >10 | T79786 | ESTs | ? |
| 23623 | >10 | T84047 | ESTs | ? |
| 23652 | >10 | T86674 | ESTs | other |
| 42242 | >10 | T89579 | Homo sapiens | other |
| 23759 | >10 | T90313 | ESTs | other |
| 23832 | >10 | T92018 | ESTs | other |
| 32740 | >10 | T92950 | ESTs | other |
| 42290 | >10 | T95105 | ESTs | ? |
| 3598 | >10 | U01157 | Glucagon-like | SS, TM |
| 3659 | >10 | U04313 | Protease inhib | other |
| 3799 | >10 | U10590 | Human MAGE | ? |
| 3870 | >10 | U14516 | Centromere p | other |
| 3913 | >10 | U16261 | Human MDA-M | SS, |
| 4029 | >10 | U21090 | Human DNA p | other |
| 4157 | >10 | U28811 | Human cystei | other |
| 4178 | >10 | U30246 | Human bume | TM |
| 15006 | >10 | U30246 | Human bume | TM |
| 4193 | >10 | U31116 | Human beta-3 | TM |
| 4308 | >10 | U36798 | Homo sapiens | TM |
| 4382 | >10 | U39817 | Bloom syndro | other |
| 4385 | >10 | U40822 | DNA repair pr | other |
| 4388 | >10 | U40714 | Human tyrosy | other |
| 4455 | >10 | U43944 | MALATE OXID | other |
| 4477 | >10 | U45980 | Human IAP-lik | other |
| 4680 | >10 | U55766 | Human Rev in | TM |
| 4702 | >10 | U57341 | EST - U57341 | other |
| 4713 | >10 | U57721 | Human L-kynu | other |
| 4787 | >10 | U61145 | Human enhan | other |
| 4862 | >10 | U65437 | Human homeo | ? |
| 4945 | >10 | U69108 | Homo sapiens | other |
| 4975 | >10 | U71088 | Human MEK5 | other |
| 4994 | >10 | U72514 | Human C2f m | other |
| 5002 | >10 | U72761 | Human karyop | other |
| 5021 | >10 | U73524 | Human putativ | TM |
| 5149 | >10 | U79716 | Human reelin | SS, |
| 5214 | >10 | U83303 | H.sapiens mR | ? |
| 5243 | >10 | U85946 | Human brain s | other |
| 32789 | >10 | W02779 | ESTs Moderat | other |
| 42354 | >10 | W19346 | ESTs | other |
| 42390 | >10 | W40150 | Homo sapiens | other |
| 33006 | >10 | W46286 | ESTs Weakly | TM |
| 33020 | >10 | W46891 | ESTs Weakly | other |
| 33109 | >10 | W59951 | Human mRNA | other |
| 24197 | >10 | W67277 | ESTs | other |
| 24215 | >10 | W69425 | ESTs | other |
| 33301 | >10 | W73883 | ESTs | other |
| 33343 | >10 | W79834 | ESTs Weakly | other |
| 33377 | >10 | W81219 | ESTs Weakly | other |
| 42602 | >10 | W85423 | ESTs | TM |
| 33556 | >10 | W90705 | Murine leukem | other |
| 33616 | >10 | W93726 | Protease inhib | other |
| 33666 | >10 | W95876 | ESTs | TM |
| 5510 | >10 | X05360 | Cell division g | ? |
| 5558 | >10 | X07876 | Wingless-type | SS, |
| 5603 | >10 | X14253 | Teratocarcino | TM |

FIGURE 12 (cont.)

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| | | | | |
|-------|-------------|---------------|----------------|--------|
| 5619 | >10 | X14650 | HISTONE H2A | SS, |
| 5623 | >10 | X14975 | T-CELL SURF | ? |
| 5692 | >10 | X17644 | G1 to S phase | other |
| 5789 | >10 | X54925 | Matrix metallo | other |
| 5799 | >10 | X55330 | Aspartylglucos | SS, |
| 5802 | >10 | X55544 | CYCLOC-AMF | ? |
| 5857 | >10 | X58377 | Human mRN | other |
| 5960 | >10 | X63575 | ATPase Ca++ | TM |
| 5963 | >10 | X63629 | Cadherin 3 (P | SS, TM |
| 5986 | >10 | X64810 | Proprotein con | ? |
| 6041 | >10 | X67155 | MITOTIC KIN | other |
| 6095 | >10 | X69962 | Fragile X mer | other |
| 6100 | >10 | X70583 | SRY (sex dele | TM |
| 6155 | >10 | X74331 | DNA primase | other |
| 6187 | >10 | X74987 | Ribonuclease | other |
| 6188 | >10 | X76029 | NEUROMEDI | TM |
| 6315 | >10 | X81889 | H.sapiens mR | other |
| 6382 | >10 | X85133 | H.sapiens RE | other |
| 6384 | >10 | X85137 | Human kines | other |
| 6438 | >10 | X86398 | URACIL-DNA | ? |
| 6449 | >10 | X89986 | H.sapiens mR | TM |
| 6478 | >10 | X91848 | H.sapiens mR | SS, TM |
| 6479 | >10 | X91853 | EST - X91853 | ? |
| 6494 | >10 | X92689 | H.sapiens mR | TM |
| 6713 | >10 | Y08584 | EST - Y08584 | ? |
| 6790 | >10 | Y12394 | Homo sapiens | other |
| 24915 | >10 | YEL003w/ | EST - YEL003 | ? |
| 42773 | >10 | YEL019c/MMEST | EST - YEL019 | ? |
| 24545 | >10 | Z38462 | ESTs | other |
| 33713 | >10 | Z39427 | ESTs | other |
| 33791 | >10 | Z40883 | ESTs | other |
| 42786 | >10 | Z96394 | ESTs Moder | other |
| 21558 | >10 | R33112 | Human AF-6 m | other |
| 26718 | >10 | AA282576 | ESTs | ? |
| 40113 | .9955090945 | H78003 | ESTs | ? |
| 10801 | .9679448276 | AA069285 | ESTs Weakly | other |
| 73491 | .9513600842 | AA455239 | ESTs Highly | other |
| 23900 | .9272347693 | T95789 | ESTs | other |
| 254 | .9198395324 | D14657 | Human mRNA | other |
| 6885 | .8970927914 | Z29331 | Ubiquitin-con | other |
| 29693 | .8850766398 | H97819 | ESTs | SS, |
| 26482 | .8765189024 | AA262491 | ESTs | other |
| 23123 | .8699502035 | T25306 | EST | ? |
| 26525 | .8160399123 | AA278392 | ESTs | other |
| 13110 | .7643356605 | AA435840 | Homo sapiens | other |
| 34863 | .7067597628 | AA299784 | EST | other |
| 39432 | .7034550083 | D51691 | Phosphoribos | ? |
| 31312 | .6513325386 | N66845 | ESTs Weakly | ? |
| 21112 | .6358446348 | R01179 | ESTs | ? |
| 31572 | .6254820695 | N71294 | ESTs | other |
| 17903 | .6221229756 | AA160259 | EST | ? |
| 20747 | .6094813734 | N68842 | ESTs | other |
| 4676 | .9589223908 | U55206 | Homo sapiens | TM |
| 34363 | .5627081023 | AA251587 | Homo sapiens | other |
| 39094 | .9540768986 | AA620636 | ESTs | other |
| 3888 | .5372000133 | U15128 | Human beta-1 | ? |

FIGURE 12
(cont.)

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| | | | | |
|-------|--------------|------------|-----------------|-------|
| 39386 | 9.506250529 | D12184 | ESTs | TM |
| 7674 | 4.458059039 | AA203742 | ESTs | other |
| 4192 | 4.329744134 | U31099 | Human DP pr | TM |
| 4507 | 9.422674945 | U47050 | Human putativ | TM |
| 35606 | 9.412026255 | AA402227 | ESTs Modera | other |
| 4970 | 3.649551013 | U70862 | Human nuclea | ? |
| 19829 | 3.432151573 | H56613 | EST | ? |
| 14837 | 2.878584144 | T40145 | ESTs | TM |
| 17336 | 2.822148679 | AA099595 | ESTs | other |
| 40541 | 2.532836505 | N30160 | ESTs | other |
| 29496 | 2.487643833 | H65434 | EST | ? |
| 29943 | 1.797074262 | N24786 | ESTs Modera | TM |
| 17997 | 1.629981314 | AA169633 | EST | other |
| 21320 | 1.243463318 | R11673 | ESTs | other |
| 13683 | 1.117879563 | AA478917 | ESTs Weakly | other |
| 30539 | 0.886887776 | N49072 | ESTs | other |
| 32778 | 0.877919548 | W02063 | EST | ? |
| 26380 | 0.809559378 | AA257012 | EST | ? |
| 15888 | 0.595893607 | X95632 | Human Abl in | other |
| 40812 | 0.012874244 | N83419 | ESTs | other |
| 903 | 9.640387908 | D90070 | ATL-derived P | other |
| 22674 | 9.515777733 | R87160 | ESTs | TM |
| 40807 | 9.510132268 | N62995 | TRANSCRIP | other |
| 15244 | 9.195844974 | W00904 | ESTs | TM |
| 32295 | 8.658779567 | R67075 | Zinc finger pro | other |
| 18299 | 8.675856795 | AA209487 | ESTs | other |
| 19562 | 8.607626284 | H47391 | ESTs | other |
| 41607 | 8.833925517 | R67868 | CLEAVAGE S | other |
| 2548 | 8.299804899 | M25897 | Platelet factor | TM |
| 7736 | 8.279341243 | AA232121 | Human tyros | other |
| 34490 | 7.844537272 | AA262354 | ESTs | other |
| 38656 | 7.669313482 | AA599477 | ESTs | other |
| 7528 | 8.765157554 | AA149543 | ESTs | other |
| 39939 | 7.555031142 | H53454 | EST - RC_H5 | other |
| 25111 | 7.232692309 | AA020787 | ESTs | other |
| 21655 | 8.718167279 | R38239 | EST | ? |
| 39503 | 8.655982852 | H04755 | ESTs Highly | other |
| 1042 | 8.652112324 | HG2510-HT2 | EST - HG2510 | ? |
| 23230 | 8.6361115426 | R77776 | ESTs | other |
| 25382 | 8.623945648 | AA059007 | ESTs | other |
| 27074 | 8.5900813076 | AA401475 | ESTs Weakly | SS, |
| 3955 | 8.5298909183 | U18259 | MHC class II | other |
| 4959 | 8.52646827 | U70322 | Human transp | other |
| 2315 | 8.5259185808 | M14123 | EST - M14123 | ? |
| 37253 | 8.496914632 | AA449357 | ESTs | other |
| 39624 | 8.471316877 | F10836 | ESTs | ? |
| 23213 | 8.4589920887 | T40891 | ESTs | ? |
| 2796 | 8.455596435 | M54995 | Connective tis | TM |
| 41154 | 8.441339014 | R07499 | ESTs | ? |
| 32479 | 8.4093889546 | T16282 | WEE1-LIKE P | other |
| 41251 | 8.3587565415 | R28279 | Human clone | other |
| 19081 | 8.3583603183 | H06701 | ESTs Weakly | other |
| 21098 | 8.3105927559 | R00545 | ESTs | other |
| 14723 | 8.3061679053 | D59894 | ESTs | other |
| 37154 | 8.299482234 | AA447866 | Human CENP | other |
| 8066 | 8.283558636 | AA313387 | ESTs Highly | other |

FIGURE 12
(cont.)

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| | | | | |
|-------|-------------|------------|------------------|-------|
| 7485 | 8.261679348 | AA129547 | ESTs | other |
| 16501 | .2517969634 | AA026969 | ESTs | other |
| 34527 | .2419163754 | AA270901 | ESTs | other |
| 6700 | .1948675662 | Y07867 | H.sapiens mR | other |
| 2852 | .1928816537 | M58460 | Human 75-kD | other |
| 11188 | .1862492468 | AA172372 | ESTs | TM |
| 42293 | 8.183311064 | T95333 | ESTs Weakly | TM |
| 5443 | 1.763317544 | X02630 | Interferon (gain | SS, |
| 40937 | .1534810594 | N70607 | ESTs | TM |
| 23371 | .1499496068 | T59505 | EST - RC_T59 | ? |
| 26272 | .1339974519 | AA252981 | ESTs Weakly | other |
| 17306 | .1332403762 | AA086201 | ESTs | other |
| 18497 | .1192326373 | AA233795 | ESTs | other |
| 235 | .0944363901 | D13644 | Human mRNA | other |
| 24525 | .0860187097 | Z38347 | ESTs | TM |
| 7826 | .0750029554 | AA248884 | EST - AA2488 | TM |
| 32142 | .0739258775 | R38715 | Homo sapiens | other |
| 39067 | .0557768803 | AA620405 | ESTs | other |
| 6235 | .0448957234 | X78416 | Casolin alpha | TM |
| 29517 | .0017588722 | H88261 | ESTs | other |
| 28570 | .9852455973 | C21104 | Homo sapiens | other |
| 39344 | .9162087762 | C21034 | ESTs Moderat | other |
| 18951 | .9002189759 | H00580 | ESTs | other |
| 18953 | .8709160227 | H00615 | ESTs | other |
| 18376 | .8584099916 | AA226925 | ESTs | other |
| 19830 | 7.847878447 | H58911 | ESTs | other |
| 36023 | 7.840835828 | AA416881 | ESTs | other |
| 13347 | .8344414518 | AA449238 | ESTs | other |
| 36614 | .8284591351 | AA431465 | ESTs | other |
| 2192 | .8254072032 | L48211 | Homo Sapien | ? |
| 33018 | .8008574086 | W48577 | H.sapiens mR | other |
| 17215 | .7941954036 | AA083044 | ESTs | other |
| 34894 | .7659738105 | AA311881 | EST | ? |
| 40614 | 7.695001222 | N39257 | ESTs | other |
| 36295 | .6834749896 | AA424534 | ESTs | other |
| 19564 | .6744302768 | H38833 | ESTs | TM |
| 16914 | .6686405336 | AA058665 | ESTs | SS, |
| 35967 | .6378079107 | AA412694 | Human splicin | other |
| 21672 | .6364823402 | R38635 | ESTs | other |
| 19918 | .6303275831 | H69787 | ESTs | ? |
| 10511 | .6297744492 | AA024462 | ESTs Highly | other |
| 17721 | .6057911016 | AA136590 | ESTs | ? |
| 42302 | .6031859697 | T96130 | EST | SS, |
| 26134 | .6000619383 | AA243763 | ESTs | other |
| 18766 | .5621799006 | F09497 | ESTs | other |
| 34492 | 7.501590494 | AA262439 | ATL derived p | other |
| 270 | .4512152125 | D14822 | EST - D14822 | other |
| 35975 | .4177746986 | AA412738 | ESTs | other |
| 29842 | .4095809671 | N21688 | ESTs | ? |
| 35389 | .3913043319 | AA399555 | ESTs | ? |
| 19979 | .3668157166 | H86477 | ESTs | other |
| 5793 | .3665664025 | X54942 | CDC28 protei | other |
| 19976 | 7.380959715 | H87770 | EST - RC_H8 | other |
| 1280 | .3691089318 | HG4126-HT4 | EST - HG4126 | ? |
| 31571 | .3676263454 | N71250 | ESTs | other |
| 23765 | .3541191734 | T90443 | ESTs Weakly | ? |

FIGURE 12
(cont.)

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| | | | | |
|-------|-------------|------------|----------------|-------|
| 35123 | .3397933454 | AA380827 | EST | ? |
| 38252 | .3341119467 | AA489247 | ESTs | other |
| 38216 | .3282021037 | AA488861 | ESTs | other |
| 29418 | .2489407005 | H77915 | EST - RC_H7 | ? |
| 4834 | .1980951054 | U63541 | Human mRNA | other |
| 42504 | .1913036522 | W69803 | ESTs | other |
| 6111 | .7158000198 | X71125 | H.sapiens mR | TM |
| 41773 | .7154479618 | T03024 | ESTs Weakly | other |
| 9951 | .1363626368 | N71513 | ESTs | other |
| 28109 | .0941968224 | AA485212 | ESTs | other |
| 988 | .0783044659 | HG2160-HT2 | EST - HG2160 | ? |
| 29848 | .0610668511 | N22107 | ESTs | other |
| 30628 | .0607950168 | N50744 | ESTs | other |
| 22567 | .0225726353 | R77771 | ESTs | TM |
| 9347 | .7006323071 | H03686 | ESTs | TM |
| 11696 | .0026773299 | AA252894 | ESTs | other |
| 40584 | .0010096333 | N34870 | EST | ? |
| 193 | .9767029168 | D10923 | PROBABLE G | TM |
| 18305 | .9740536051 | AA214048 | Collagen type | other |
| 6078 | .9699682397 | X69141 | FARNESYL-D | other |
| 26741 | .6902658703 | AA283198 | ESTs | other |
| 35069 | .8992865685 | AA358397 | EST | ? |
| 23504 | .8977135983 | T71042 | ESTs | other |
| 299 | .8824513028 | D18815 | Homo sapiens | other |
| 40583 | .888903023 | N34855 | ESTs | other |
| 31428 | .8623762224 | N68594 | ESTs | other |
| 6169 | .8606959727 | X75091 | SET PROTEIN | other |
| 39524 | .8567355177 | F01905 | MALATE OXID | other |
| 34578 | .8430689439 | AA260837 | ESTs | other |
| 38678 | .6837527995 | AA599920 | Small inducib | other |
| 23936 | .8251471804 | T96930 | ESTs | other |
| 9326 | .8181321394 | D89377 | Msh (Drosoph | other |
| 19188 | .8067351963 | H11255 | ESTs Highly | TM |
| 18185 | .7882148811 | AA194983 | Homo sapiens | other |
| 27028 | .6757529124 | AA399630 | ESTs Weakly | other |
| 41289 | .751953168 | R37265 | EST | other |
| 34511 | .7364448798 | AA278298 | EST - RC_AA | other |
| 1566 | .7056207716 | J05614 | EST - J05614 | ? |
| 25675 | .6692296748 | AA129757 | ESTs Highly | other |
| 5814 | .6584342828 | X56088 | CYTOCHROM | SS, |
| 13861 | .6236291607 | AA470145 | ESTs | other |
| 29794 | .6026313352 | N20598 | ESTs | other |
| 39333 | .5902382643 | C20910 | Cyclin B1 | other |
| 3770 | .5835303599 | U09609 | Nuclear factor | other |
| 31831 | .5629933764 | N89894 | ESTs | ? |
| 33063 | .5808125026 | W53000 | Homo sapiens | other |
| 20326 | .5640084836 | N35583 | ESTs Weakly | ? |
| 34384 | .5535703492 | AA252537 | ESTs | other |
| 25599 | .5490481997 | AA114091 | Human (clone | other |
| 39749 | .5369363254 | H14988 | ESTs | other |
| 42596 | .5200567072 | W85900 | ESTs | ? |
| 39606 | .5119482185 | F10243 | ESTs Weakly | ? |
| 14617 | .5105504748 | C14983 | ESTs | other |
| 27831 | .645670814 | AA456044 | ESTs | ? |
| 34896 | .4496517783 | AA312551 | EST | ? |
| 27360 | .4434305006 | AA425356 | ESTs | other |

FIGURE 12 (cont.)

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| | | | | |
|-------|-------------|------------|----------------|-------|
| 20126 | .4326610424 | N22015 | ESTs | TM |
| 6663 | .4324809977 | Y00291 | RETINOIC AC | TM |
| 30692 | .4196636207 | N51563 | ESTs | other |
| 36472 | .4189542268 | AA428633 | EST | ? |
| 9578 | .3961788753 | H87652 | Homo sapiens | other |
| 39670 | .3818496159 | H05626 | ESTs | other |
| 22697 | .3652792447 | R89218 | ESTs | other |
| 37308 | .3647904993 | AA451694 | EST | TM |
| 16101 | .3517262802 | AA002147 | EST | ? |
| 20629 | .348685440 | N59798 | ESTs | other |
| 36100 | .3364146287 | AA417740 | ESTs | ? |
| 15498 | .3252590241 | W28097 | Homo sapiens | other |
| 36667 | .3131273544 | AA432136 | ESTs | other |
| 30766 | .3115037924 | N52627 | EST - RC_N5 | ? |
| 32882 | .2745311453 | W37683 | ESTs | TM |
| 18072 | .2675797205 | AA180448 | EST | ? |
| 18231 | .2652604663 | AA189747 | Human mRNA | other |
| 38282 | .2514165678 | AA469814 | EST | ? |
| 28125 | .6250317021 | AA466073 | ESTs | other |
| 37464 | .2484456382 | AA454747 | ESTs | ? |
| 36618 | .1946328223 | AA431478 | ESTs | other |
| 5082 | .1931116815 | U78524 | Human Gu bin | other |
| 1441 | .1777287039 | J02953 | Integrin alpha | other |
| 42105 | .614875944 | T67710 | ESTs | ? |
| 8081 | .1394863141 | X68314 | Glutathione pe | SS, |
| 32570 | .1158028796 | T30222 | ESTs Weakly | TM |
| 32504 | .1019612076 | T17063 | EST | ? |
| 23335 | .0977927504 | T56804 | EST | ? |
| 10867 | .0970991075 | AA088458 | ESTs Weakly | other |
| 30883 | .0911993489 | N56923 | EST | ? |
| 14528 | .0859008453 | AA620295 | ESTs | TM |
| 29454 | .0685955036 | H81308 | EST | ? |
| 6798 | .0539173278 | Y13153 | Homo sapiens | TM |
| 21248 | .0525426546 | R08871 | ESTs | ? |
| 21940 | .0499964138 | R44538 | ESTs | ? |
| 29066 | .0455247653 | F10927 | Homo sapiens | other |
| 18774 | .0446826953 | F09609 | ESTs | ? |
| 36722 | .0172343991 | AA435512 | ESTs | SS, |
| 18062 | .0034342966 | AA179845 | ESTs Modera | other |
| 22969 | .9992817406 | T16305 | ESTs | other |
| 41745 | .9905623898 | R95995 | ESTs | ? |
| 8787 | .9894877658 | AA504307 | X-LINKED HE | other |
| 20550 | .5984861795 | N55013 | ESTs | other |
| 26470 | .9417764101 | AA262179 | ESTs | other |
| 16574 | .9356497566 | AA031926 | EST | other |
| 693 | .9169537385 | D80007 | Human mRNA | other |
| 4093 | .5191830973 | U25182 | Human anilox | TM |
| 1192 | .9086264407 | HG3546-HT3 | EST - HG3546 | ? |
| 22956 | .8954735623 | T10248 | ESTs | other |
| 36723 | .5891606409 | AA435524 | EST | ? |
| 2114 | .8944986598 | L40384 | EST - L40384 | other |
| 26872 | .5868238789 | AA291137 | ESTs | other |
| 6602 | .8663853018 | X98266 | EST - X98266 | other |
| 42701 | .8594493433 | Z38612 | ESTs | other |
| 28573 | .5845911116 | C21118 | ESTs | other |
| 18290 | .8189427593 | AA211901 | ESTs | other |

FIGURE 12
(cont.)

| | | | | |
|-------|------------|-------------------------|----------------|-------|
| 7320 | 8043917941 | D083781 | Human mRNA | ? |
| 5300 | 801414561 | U919327 | EST - UB9327 | ? |
| 33503 | 7990715189 | W88720 | EST | ? |
| 2553 | 7797505884 | M62167 | Human platelet | ? |
| 34505 | 7658806254 | AA286907 | ESTs Weakly | other |
| 42655 | 7549409104 | W93659 | ESTs | other |
| 28185 | 7539310793 | AA4887495 | EST - RC_AA | other |
| 4244 | 7476738809 | U33286 | Human chrom | other |
| 32822 | 7418957453 | W16634 | ESTs | TM |
| 3977 | 7245885557 | U19991 | Retinal pigme | ? |
| 24673 | 7202636615 | 238301 | ESTs | TM |
| 6928 | 7120261128 | 246629 | SRY (sex-dete | other |
| 38726 | 7030796258 | AA068733 | ESTs | other |
| 39290 | 6892320758 | U14573 | Human mRNA | other |
| 11405 | 6818873796 | AA232321 | ESTs | other |
| 22538 | 6792006599 | R73567 | Homo sapiens | TM |
| 40573 | 6605338208 | N56872 | ESTs | other |
| 31596 | 6554024604 | H72094 | ESTs | other |
| 6329 | 6415652518 | K82279 | EST - X82279 | ? |
| 31578 | 627333266 | W11361 | ESTs | other |
| 33207 | 6271814867 | W70051 | H.sapiens mR | other |
| 2545 | 6105866104 | K42573 | Cyclin B1 | other |
| 22480 | 5988402547 | R79156 | ESTs | other |
| 33592 | 5935314518 | W93127 | ESTs | other |
| 28843 | 5734698758 | D60252 | ESTs | other |
| 6180 | 5680506518 | X77494 | ODC2?1 HOMO | other |
| 37967 | 5561345667 | AA479665 | ESTs | other |
| 42515 | 521786861 | W127216 | Homo sapiens | other |
| 4732 | 5130686523 | U58522 | Human huntu | other |
| 3299 | 5098950678 | K495623 | Hydroxymethy | ? |
| 26320 | 5473040681 | AA599574 | ESTs | ? |
| 746 | 5471260899 | D84454 | Human mRNA | TM |
| 39373 | 4635804954 | C21517 | ESTs | other |
| 2117 | 4398413537 | M81182 | Peroxisomal m | other |
| 31257 | 434361241 | R09196 | ESTs Modera | other |
| 31487 | 4318648859 | N08057 | ESTs | other |
| 28954 | 4137130511 | F03153 | ESTs | other |
| 38928 | 5369782771 | AA609995 | ESTs | other |
| 22903 | 372320622 | N23366 | EST | ? |
| 39025 | 343732318 | N58295 | ESTs Weakly | ? |
| 10991 | 3344615608 | H07864 | ESTs | TM |
| 28209 | 3138951918 | AA491250 | ESTs | other |
| 9470 | 3118897984 | H46617 | EST - H46617 | ? |
| 9435 | 3070056656 | J30201 | EST - J30201 | other |
| 28552 | 2954432572 | C20914 | ESTs | other |
| 27811 | 2940164287 | AA428137 | ESTs | other |
| 30615 | 2924125258 | N50556 | ESTs | other |
| 2813 | 2657977167 | AA599309 | ESTs | TM |
| 39321 | 2649035334 | C26032 | ESTs | ? |
| 29924 | 2531047399 | N24194 | ESTs | other |
| 28464 | 2496703122 | HG2846-H72E-ST - HG2846 | ESTs | TM |
| 39578 | 2481126334 | H08925 | ESTs | other |
| 11232 | 2466795424 | AA196804 | ESTs Weakly | other |
| 12426 | 2426349328 | M21539 | Human small | other |
| 26843 | 2387758661 | AA287450 | ESTs | ? |
| 40331 | 2353585567 | H97562 | ESTs Weakly | ? |

FIGURE 12
(cont.)

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| | | | | |
|-------|-------------|------------|-----------------|--------|
| 8035 | 5.205798365 | AA305116 | EST - AA3051 | other |
| 29793 | 1955425722 | N20593 | ESTs Weakly | other |
| 34109 | 1481590107 | AA210722 | EST | ? |
| 26408 | 1432577257 | AA258177 | ESTs Weakly | other |
| 19263 | 1427029807 | H15054 | ESTs | TM |
| 24596 | 1416089352 | Z38810 | ESTs | other |
| 28589 | 1365059753 | C21245 | H.sapiens mF | other |
| 5684 | 1121931412 | X17098 | Pregnancy-sp | other |
| 30710 | 1079347344 | N51761 | EST | ? |
| 35765 | 0973514948 | AA406167 | EST | ? |
| 26360 | 0863127861 | AA256460 | ESTs | ? |
| 2351 | 0849612092 | M15796 | Proliferating C | ? |
| 30282 | 0636877534 | N35065 | Homo sapiens | other |
| 41792 | 0737512468 | T03886 | ESTs | ? |
| 36710 | 0703839854 | AA434411 | ESTs | other |
| 39090 | 0546865407 | AA620628 | ESTs | TM |
| 42185 | 0539926381 | T79951 | ESTs | ? |
| 18745 | 0480321557 | F09134 | ESTs | other |
| 35746 | 0396841996 | AA406063 | ESTs | other |
| 35356 | 0354809581 | AA399053 | EST | ? |
| 36769 | 0312706878 | AA435750 | EST | ? |
| 36900 | 0279911548 | AA436866 | H.sapiens mF | other |
| 27595 | 0244757301 | AA443328 | ESTs | TM |
| 16290 | 0056811904 | AA016145 | ESTs | ? |
| 27117 | 0016146598 | AA405098 | ESTs Weakly | other |
| 4304 | 9951954397 | U36784 | Eukaryotic tra | other |
| 33458 | 9807402071 | W98835 | Homo sapiens | other |
| 26693 | 9800090679 | AA282120 | EST | ? |
| 12669 | 9758136851 | AA417030 | Homo sapiens | other |
| 29701 | 9708526387 | H97870 | EST | ? |
| 20480 | 9557253638 | N52168 | ESTs | TM |
| 8720 | 9439110602 | AA481218 | EST - AA4812 | other |
| 34628 | 9431269473 | AA292436 | Homo sapiens | SS, TM |
| 14985 | 4.941621032 | U15128 | Human beta-1 | ? |
| 16115 | 9377553522 | AA004420 | ESTs | ? |
| 42506 | 9348587118 | W70074 | EST | other |
| 34761 | 9316837445 | AA287833 | ESTs | other |
| 11870 | 9281056201 | AA262587 | ESTs | TM |
| 23211 | 9258391854 | T40889 | ESTs | other |
| 40611 | 9160502273 | N39138 | Homo sapiens | other |
| 42811 | 9128605354 | W87006 | Homo sapiens | other |
| 39652 | 9045174605 | H03099 | ESTs | other |
| 17581 | 4.889674751 | AA129395 | EST | ? |
| 37239 | 8704375383 | AA449121 | ESTs | ? |
| 18712 | 8703618781 | F04677 | ESTs | other |
| 30709 | 8611171953 | N51752 | ESTs Weakly | other |
| 34179 | 8503613948 | AA227903 | ESTs Highly | other |
| 21433 | 4.825670988 | R22183 | EST | ? |
| 39731 | 8186142741 | H11750 | ESTs | other |
| 31295 | 8116614607 | N66653 | ESTs | other |
| 24647 | 4.804163055 | Z39108 | EST | ? |
| 31292 | 8008871817 | N66615 | ESTs | other |
| 1285 | 7997542393 | HG4157-H14 | EST - HG4157 | ? |
| 1106 | 7932425855 | HG2981-H13 | EST - HG2981 | ? |
| 18212 | 7912262563 | AA196506 | ESTs | other |
| 34367 | 4.782207045 | AA251758 | Homo sapiens | other |

FIGURE 12
(cont.)

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| | | | | |
|-------|------------|----------|-----------------|--------|
| 34802 | 7797760205 | AA291458 | ESTs | TM |
| 34762 | 7775301546 | AA287834 | ESTs | other |
| 11595 | 7696612948 | AA242819 | ESTs | other |
| 8295 | 7639639111 | AA405082 | ESTs | ? |
| 17622 | 4758635576 | AA131584 | ESTs Weakly | other |
| 35781 | 7572463523 | AA406335 | ESTs | other |
| 34754 | 7483874972 | AA287842 | Human mRNA | other |
| 23237 | 7444854356 | T47291 | EST | ? |
| 37667 | 7280445357 | AA460318 | ESTs Highly | other |
| 11568 | 7257189975 | AA236786 | ESTs | other |
| 38622 | 7190695733 | AA598967 | ESTs | ? |
| 5137 | 7057359474 | U79296 | Dihydrolipoam | other |
| 25038 | 7002244728 | AA010065 | CDC28 protein | other |
| 19288 | 7000147312 | H16567 | ESTs | other |
| 32503 | 6879488292 | T17045 | Collagen type | other |
| 3276 | 6853739298 | M94055 | SODIUM CHA | TM |
| 9696 | 6642061018 | L38961 | Integral transm | TM |
| 35400 | 6601390898 | AA399591 | Homo sapiens | other |
| 35246 | 6662691303 | AA398367 | EST Weakly | ? |
| 36387 | 6622499271 | AA426270 | ESTs | other |
| 21509 | 6730072542 | R27314 | ESTs | other |
| 31381 | 6729672124 | N67889 | ESTs | other |
| 26723 | 6727894928 | AA282871 | ESTs Highly | other |
| 36326 | 6703621088 | AA425151 | Human GAP S | other |
| 17409 | 6688418667 | AA113136 | EST - RC_AA | other |
| 4908 | 6552339933 | U67156 | Human mitoch | other |
| 30594 | 6496238328 | N49967 | ESTs | other |
| 38286 | 484639735 | AA489947 | ESTs Weakly | ? |
| 13073 | 6426509458 | AA433950 | ESTs | other |
| 40435 | 6240181068 | N21814 | Homo sapiens | other |
| 14474 | 6228694378 | AA609427 | ESTs Modera | other |
| 38213 | 4615309907 | AA488847 | ESTs Weakly | ? |
| 5312 | 4606844198 | U90716 | Human cell su | SS, TM |
| 24225 | 6041550358 | W70328 | ESTs | ? |
| 35688 | 5868982366 | AA401750 | EST | ? |
| 29739 | 5863199051 | H99626 | EST | ? |
| 7203 | 5792992577 | AA053096 | EST - AA0530 | other |
| 2157 | 5772055865 | L41939 | Homo sapiens | SS, TM |
| 32086 | 5661024279 | R11510 | ESTs | ? |
| 8085 | 5648114738 | AA314779 | ESTs Weakly | SS, |
| 224 | 5622018988 | D13633 | Human mRNA | other |
| 34006 | 5609580241 | AA188761 | DNA polymera | other |
| 33655 | 5567384388 | W95477 | ESTs | other |
| 34065 | 5537335124 | AA195517 | ESTs Weakly | TM |
| 6028 | 5357922097 | X68503 | Adenylosuccin | other |
| 4166 | 5032930671 | U29453 | Cytochrome B | ? |
| 40262 | 5024727522 | H93562 | ESTs | TM |
| 22687 | 5018672549 | R88200 | ESTs | TM |
| 41056 | 4977510482 | N93969 | H. sapiens mR | SS, |
| 8264 | 4793100575 | AA401334 | ESTs | other |
| 27588 | 4472017297 | AA443187 | ESTs | other |
| 35882 | 4717567552 | AA412047 | ESTs | ? |
| 34476 | 4465519191 | AA252080 | Human burnt | TM |
| 15921 | 4548516436 | Y12065 | Homo sapiens | ? |
| 11275 | 4380038671 | AA195399 | ESTs | other |
| 39222 | 4387650786 | AA621348 | ESTs Highly | other |

FIGURE 12 (cont.)

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| | | | | |
|-------|-------------|----------------------|-----------------|-------|
| 34428 | .4364736766 | AA258526 | ESTs | other |
| 8771 | .432067373 | AA491188 | ESTs | other |
| 22193 | .4189610024 | R53891 | Homo sapiens | other |
| 7988 | .4066170674 | AA263032 | ESTs | other |
| 19902 | .3886145805 | H66736 | ESTs | other |
| 9276 | .3868085205 | D82374 | ESTs | other |
| 10716 | .3794529068 | AA053319 | ESTs | TM |
| 13193 | .3751913512 | AA442763 | ESTs Highly | other |
| 5690 | .3723059417 | X17620 | NUCLEOSIDE | other |
| 35102 | .4371471138 | AA371509 | EST - RC AA | TM |
| 17983 | .3612985467 | AA169226 | ESTs | other |
| 24952 | .3497206925 | AFFX-HUMTFAFFX-HUMTF | | ? |
| 31680 | .3416539683 | N74438 | ESTs | other |
| 27168 | .4330306894 | AA410258 | ESTs | other |
| 28731 | .3231846659 | D20981 | EST | ? |
| 28348 | .3212284906 | AA608752 | ESTs | other |
| 16335 | .3019961487 | AA018587 | ESTs Weakly | ? |
| 33036 | .2915844973 | W48580 | ESTs Weakly | other |
| 30180 | .2897721825 | N33144 | ESTs | other |
| 35591 | .2895841242 | AA401758 | ESTs Weakly | SS, |
| 25340 | .2721717135 | AA054554 | EST | ? |
| 28108 | .2659103748 | AA485084 | ESTs | other |
| 38690 | .2649184307 | AA600121 | ESTs | other |
| 20203 | .2626499431 | N26853 | ESTs Moderate | other |
| 10251 | .2608760694 | R76185 | ESTs Weakly | SS, |
| 12684 | .2604192389 | AA417558 | ESTs | SS, |
| 31636 | .2509469427 | N73680 | Natural resista | TM |
| 20769 | .2479765348 | N67277 | ESTs | other |
| 1572 | .2353281083 | K01884 | EST - K01884 | ? |
| 10923 | .2292322072 | AA116036 | ESTs | other |
| 34380 | .2283792392 | AA252414 | ESTs | other |
| 10132 | .2222816119 | R35733 | EST - R35733 | other |
| 16629 | .2161752119 | AA036811 | ESTs | other |
| 25146 | .1966683794 | AA026356 | ESTs | ? |
| 28730 | .1958943098 | D20959 | ESTs Moderate | other |
| 10200 | .1874912391 | R64521 | ESTs | other |
| 38685 | .1545794663 | AA600176 | ESTs | other |
| 31365 | .4150549979 | N67550 | ESTs | other |
| 42379 | .1496120668 | W37999 | ESTs | other |
| 28050 | .1428703354 | AA479139 | Acid phosphat | other |
| 2620 | .1385565707 | M29474 | Human recom | ? |
| 8927 | .1340593744 | AF008442 | Homo sapiens | other |
| 13379 | .1269549188 | AA449741 | ESTs Weakly | other |
| 5134 | .1218251808 | U79293 | Human clone | other |
| 2625 | .41213948 | M29581 | Zinc finger pro | other |
| 38005 | .1150483666 | AA479969 | ESTs | other |
| 36575 | .1127198584 | AA431085 | EST | ? |
| 18296 | .1121837207 | AA213620 | ESTs Weakly | ? |
| 29531 | .1111459313 | H88953 | EST - RC H8 | TM |
| 143 | .1095880506 | AFFX-HUMTFAFFX-HUMTF | | ? |
| 10970 | .0957613396 | AA129390 | ESTs | other |
| 25836 | .0952825397 | AA152305 | Interferon (gam | SS, |
| 19735 | .0937927853 | H53038 | EST | ? |
| 40711 | .0909709431 | N53654 | ESTs | other |
| 4149 | .0901471427 | U28386 | RAG (recomb | TM |
| 5767 | .0862784557 | X53793 | MULTIFUNCT | other |

FIGURE 12
(cont.)

| | | | | |
|-------|--------------|-----------|-----------------|--------|
| 5503 | 0861033575 | X05232 | Stromelysin | SS |
| 20310 | 0647111656 | X34893 | EstS Highly | SS |
| 456 | 0599824568 | D38145 | Prostaglandin | SS |
| 7814 | 0556835576 | X248406 | EstS | SS |
| 40230 | 0447282179 | H90161 | EstS | SS |
| 33651 | 4039204048 | W95049 | EstS | other |
| 16777 | 0231657929 | A0045968 | EST | ? |
| 19110 | 0094905222 | H08778 | EstS | other |
| 34442 | 0077010358 | X2259093 | HKR-T1 | other |
| 5099 | 4040992433 | U79247 | Human clone | Ther |
| 8209 | 9990473163 | X3384220 | EstS | other |
| 24408 | 9785680674 | W90146 | EstS | other |
| 26596 | 9749197874 | X2779943 | EstS | other |
| 16485 | 9611264008 | A0026269 | Spleen focus | other |
| 32969 | 9604901745 | W42541 | EstS | TM |
| 27006 | 9799705093 | X3398955 | EstS Weakly | Ther |
| 29009 | 9526756967 | N21043 | EST | other |
| 9596 | 9440153451 | H91594 | EstS | TM |
| 29024 | 9377933938 | F09315 | Homo sapiens | other |
| 21694 | 9356356584 | R39317 | Homo sapiens | other |
| 13207 | 3929990104 | AA443321 | EstS | other |
| 37865 | 9143752624 | AA476623 | EstS Highly | ? |
| 36201 | 9129281724 | AA421164 | EstS | ? |
| 8961 | 8981160286 | AFX-HUMT6 | AFX-HUMT6 | other |
| 17444 | 8927133917 | AA115933 | EstS | ? |
| 25869 | 8919834522 | AA157267 | EstS Highly | TM |
| 24692 | 3.90402522 | Z41415 | EstS Highly | other |
| 62305 | 3.893633062 | AA281950 | EstS | ? |
| 46380 | 3.8220303676 | T98550 | EstS | ? |
| 6495 | 8330844683 | Z92715 | Zinc finger pro | other |
| 38604 | 8328045942 | AA598903 | EstS | TM |
| 36358 | 8326713718 | AA425756 | EstS | other |
| 30580 | 3.732784456 | U48284 | MYB PROTO- | other |
| 14413 | 8724486156 | AA601150 | EstS | other |
| 23823 | 8574022967 | T91805 | Homo sapiens | other |
| 38158 | 3.835996838 | AA478021 | EST | ? |
| 2572 | 8519747554 | M27281 | Vascular endo | other |
| 40100 | 8464108967 | H75933 | Laminin recep | other |
| 40256 | 8462992993 | H93340 | EstS | TM |
| 20944 | 8461621522 | N74433 | EstS | other |
| 20411 | 8459409058 | H49863 | Homo sapiens | other |
| 10345 | 8457714481 | AA001663 | EstS | other |
| 31261 | 8451974147 | N66246 | EST | other |
| 8513 | 8378410994 | AA449990 | EstS | other |
| 13877 | 8363409935 | AA476804 | EstS | other |
| 40748 | 8253562321 | N56879 | EST | ? |
| 14509 | 8152852193 | AA609943 | EstS | other |
| 10261 | 8065567331 | R003333 | EstS | other |
| 25284 | 8044156642 | AA045074 | EstS Weakly | other |
| 6730 | 7900025129 | T09305 | H.sapiens mR | other |
| 16033 | 7884592402 | AFX-HUM15 | AFX-HUM15 | other |
| 19422 | 7827164806 | AA545253 | EstS | ? |
| 23554 | 7794760434 | AA425221 | EstS | ? |
| 47552 | 3.777263955 | U49188 | Human placen | SS, TM |
| 18355 | 7756191990 | AA227219 | Homo sapiens | other |
| 16786 | 7677416053 | AA040607 | EST - RC AA | other |

FIGURE 12
(cont.)

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| | | | |
|-------|-------------|----------|---------------|
| 12752 | .7671137403 | AA421250 | ESTs |
| 42463 | .7601033106 | W60180 | ESTs |
| 10614 | .7581669016 | AA037357 | ESTs |
| 867 | .7459337968 | D87716 | Human mRNA |
| 7608 | .7336047135 | AA180987 | ESTs |
| 31795 | .737328742 | N80703 | ESTs |
| 35377 | .7273784603 | AA389453 | EST - RC_AA |
| 22828 | .7243928524 | R98182 | ESTs |
| 25240 | .7243198336 | AA039713 | ESTs |
| 11008 | .7197381366 | AA134289 | ESTs Weakly |
| 4341 | .7162349944 | U38545 | Human ARF-a |
| 28833 | .7147818393 | D58787 | EST - RC_D6 |
| 3750 | .7121007154 | U08279 | Collagen type |
| 17483 | .6943413512 | AA122147 | ESTs |
| 16854 | .691520847 | AA055552 | ESTs Weakly |
| 3709 | .689165677 | U07550 | Heat shock 10 |
| 1608 | .6652978422 | L00205 | KERATIN TYP |
| 24577 | .6617721053 | Z38727 | Homo sapiens |
| 31032 | .6570916386 | N62508 | ESTs |
| 4951 | .6536195433 | U69546 | Human RNA p |
| 37680 | .6523275307 | AA460225 | ESTs |
| 20418 | .648635708 | N46209 | ESTs |
| 27995 | .6486187436 | AA470155 | Homo sapiens |
| 7971 | .6434397185 | AA287423 | ESTs |
| 27608 | .634303453 | AA443793 | ESTs |
| 24677 | .6427250833 | Z38338 | ESTs Highly |
| 11070 | .6406198277 | AA148521 | ESTs Weakly |
| 9328 | .6356048599 | D89818 | Homo sapiens |
| 36826 | .6344889602 | AA435996 | ESTs |
| 17676 | .6300045795 | AA134275 | Human HIV1 |
| 36209 | .6274694477 | AA421266 | ESTs Weakly |
| 34120 | .6258090412 | AA211615 | EST |
| 38152 | .6246442011 | AA486737 | H.sapiens mR |
| 38463 | .6184893256 | AA504491 | ESTs Weakly |
| 20064 | .6183099976 | H98053 | ESTs |
| 31256 | .5982620732 | N86152 | EST |
| 9713 | .5985228843 | L44338 | Homo sapiens |
| 28622 | .5768056147 | D11837 | ESTs |
| 38057 | .5736105703 | AA481549 | EST - RC_AA |
| 28763 | .5688723791 | D45568 | EST |
| 16996 | .5680705709 | AA069038 | EST - RC_AA |
| 28628 | .5604144617 | D11888 | ESTs Modera |
| 25804 | .5442954572 | AA148885 | ESTs |
| 2492 | .5423964239 | M22898 | Tumor protein |
| 14904 | .5411970737 | T83389 | ESTs Highly |
| 25265 | .5347588502 | AA043765 | H.sapiens RY |
| 13606 | .5327912417 | AA465437 | ESTs Weakly |
| 42307 | .5318436465 | T96595 | EST - RC_T96 |
| 1544 | .3526202414 | J05068 | TRANSCOBA |

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FIGURE 12
(cont.)

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| Accession | Gene | Protein | Description |
|-----------|--------|---------|---|
| Accession | Gene | Protein | Description |
| C2A8 | 111929 | 3.7 | R40557 promitin (mouse)-like 1 |
| BCK2 | 128790 | 4.0 | AA291725 secreted frizzled-related protein 4 |
| CBC2 | 101009 | 5.7 | M86849 Homo sapiens connexin 26 (Cx26) mRNA, complete cds |
| CBC1 | 100366 | 4.8 | D78611 mesoderm specific transcript (mouse) homolog |
| CBC3 | 102618 | 2.5 | U65932 extracellular matrix protein 1 |
| | 134804 | 6.3 | L37036 small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78) |
| | 104209 | 2.1 | AB000221 small inducible cytokine subfamily A (Cys-Cys), member 18; pulmonary and activation-regulated |
| CJA8 | 115597 | 8.1 | AA411602 ESTs; Weakly similar to airway trypsin-like protease (H sapiens) |
| | 124315 | 5.4 | H94892 v-rat simian leukemia viral oncogene homolog A (Ras related) |
| | 109415 | 4.3 | AA227219 Homo sapiens CACBP mRNA, partial cds |
| | 103513 | 5.1 | Z46029 SRV (sex-determining region Y) box 9 (X-chromosomal dysplasia, autosomal sex-reversal) |
| | 109156 | 6.2 | AA179845 RA36 interacting; kinesin-like (rabbithead) |
| CJA9 | 115176 | 5.7 | AA403725 ESTs; Weakly similar to KIAA0226 (H sapiens) |
| CGA7 | 116522 | 8.1 | AA331393 ESTs |
| | 125852 | 5.7 | H09290 ESTs; Weakly similar to unknown (H sapiens) |
| BCN5 | 112244 | 3.1 | R51309 ESTs |
| QQA1 | 132592 | 5.6 | AA129390 ESTs |
| BCN7 | 117280 | 5.4 | N22107 ESTs; Moderately similar to H ¹ ALU SUBFAMILY SC WARNING ENTRY H ¹ (H sapiens) |
| | 102863 | 4.8 | U70322 karyophen (importin) beta 2 |
| QQA2 | 104660 | 6.0 | AA007160 ESTs |
| | 113702 | 2.4 | T97307 ESTs; Moderately similar to H ¹ ALU SUBFAMILY J WARNING ENTRY H ¹ (H sapiens) |
| | 100154 | 6.0 | D14657 KIAA1011 gene product |
| | 102260 | 3.7 | U28395 Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds |
| | 101809 | 5.7 | M85849 Homo sapiens connexin 26 (Cx26) mRNA, complete cds |
| | 13272 | 3.2 | AA455016 ESTs; Highly similar to serine protease homolog |
| | 100265 | 4.8 | D78511 mesoderm specific transcript (mouse) homolog |
| | 126819 | 4.7 | AA305536 EST176522 Colon carcinoma (Caco-2) cell line 8 Homo sapiens cDNA 5' end, mRNA sequence |
| | 132543 | 4.6 | AA117162 ESTs; Highly similar to protein regulating cytokinesis 1 (H sapiens) |
| | 130223 | 5.5 | X53793 multifunctional polypeptide similar to SAICAR synthetase and AR carboxylase |
| | 132109 | 3.1 | AA599801 ESTs |
| | 104037 | 3.5 | AA372630 differentially expressed in hematopoietic lineages |
| | 104978 | 3.5 | AA080458 ESTs; Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY H ¹ (H sapiens) |
| | 108696 | 3.0 | AA121315 ESTs |
| | 107248 | 3.8 | D58994 ESTs |
| | 132902 | 3.4 | AA490969 ESTs |
| | 120104 | 4.0 | W66477 ESTs |
| | 128790 | 4.0 | AA291725 secreted frizzled-related protein 4 |
| | 101923 | 3.8 | S78256 HNL-mesozephi lipocatin (human, ovarian cancer cell line OCB, mRNA Partial, 534 nt) |
| | 119943 | 3.4 | W68835 coptin III |
| | 130648 | 3.9 | AA075427 ESTs |
| | 132358 | 3.5 | X60486 H4 histone family; member G |
| | 102286 | 3.2 | AA434441 frizzled (Drosophila) homolog 7 |
| | 117557 | 2.3 | N33920 diurexin |
| | 129651 | 3.3 | X06700 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) |
| | 114767 | 4.5 | AA146885 minichromosome maintenance deficient (S. cerevisiae) 4 |
| | 100335 | 3.8 | D63391 platelet-activating factor acetylhydrolase, isoform 1; gamma subunit (29KD) |
| | 134989 | 3.5 | AA226324 ESTs; Weakly similar to H ¹ ALU CLASS A WARNING ENTRY H ¹ (H sapiens) |
| | 110009 | 3.4 | H109933 ESTs |
| | 124059 | 4.0 | F13073 ESTs |
| | 104755 | 2.2 | AA024482 ESTs; Weakly similar to epidermal type I keratin (H sapiens) |
| | 107151 | 3.4 | AA021169 ESTs |
| | 132660 | 2.9 | AA188378 ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 (H sapiens) |
| | 104394 | 5.5 | H46617 yp15h1.11 Seares (zebra) 3NpHb1 Homo sapiens cDNA clone IMAGE 187921-5', mRNA sequence |
| | 117667 | 2.5 | N39214 ser-Thr protein kinase related to the myotonic dystrophy protein kinase |
| | 104954 | 3.3 | AA074514 ESTs; Moderately similar to (calfine not available 4753768) (H sapiens) |
| | 132994 | 3.7 | AA505153 ESTs |
| | 102681 | 3.7 | U72761 karyophen (importin) beta 3 |
| | 103989 | 2.2 | AA314776 ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR (H sapiens) |
| | 132103 | 2.5 | L19183 Human MAC30 mRNA, 3' end |

FIGURE 13A

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| | | | |
|--------|-----|-------------|--|
| 118695 | 3.0 | N11761 | ESTs |
| 109552 | 3.4 | HQ2167-HT29 | tyrosine kinase H31, Camp-Dependent |
| 120471 | 2.5 | AA251826 | ESTs; Moderately similar to (define not available 4580697) [H.sapiens] |
| 120547 | 4.2 | U47732 | transmembrane 4 superfamily member 3 |
| 109067 | 3.3 | AA417067 | ESTs |
| 125103 | 4.0 | T85303 | ESTs; Weakly similar to Strabismus [D.melanogaster] |
| 135243 | 3.4 | AA215333 | ESTs |
| 121457 | 2.5 | AA411440 | ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens] |
| 131216 | 2.7 | D31058 | ESTs |
| 112671 | 2.4 | T17185 | ESTs |
| 111179 | 2.1 | N67239 | ESTs |
| 123533 | 2.3 | AA608751 | ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens] |
| 105175 | 2.4 | AA186604 | ESTs; Weakly similar to unknown [S.cerevisiae] |
| 105156 | 2.7 | AA172372 | ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens] |
| 111223 | 2.5 | N68521 | ESTs; Weakly similar to neogenin [H.sapiens] |
| 132180 | 2.7 | AA405649 | fibronectin activation protein, alpha |
| 105400 | 2.1 | AA447621 | ESTs |
| 129260 | 3.1 | AA058504 | ESTs; Highly similar to (define not available 4678014) [H.sapiens] |
| 115291 | 3.9 | AA279543 | ESTs |
| 128628 | 2.1 | C14037 | ESTs; Weakly similar to Yel007-cap [S.cerevisiae] |
| 116399 | 2.7 | AA596729 | Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds |
| 130687 | 3.5 | R45898 | ESTs |
| 105082 | 2.6 | AA143763 | ESTs; Weakly similar to Similarity to S. Pombe BEM18UD5 suppressor [C.elegans] |
| 103453 | 3.2 | X56585 | H.sapiens mRNA for SM133 protein |
| 115547 | 2.6 | AA443793 | ESTs |
| 105012 | 2.8 | AA116036 | ESTs; Highly similar to (define not available 4569929) [H.sapiens] |
| 105507 | 3.2 | AA266678 | ESTs; Moderately similar to (define not available 4105051) [H.sapiens] |
| 130800 | 2.6 | AA223386 | ESTs; Weakly similar to katanin p10 subunit [H.sapiens] |
| 116461 | 3.4 | AA621557 | ESTs; Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY [H] [H.sapiens] |
| 129545 | 2.5 | AA252104 | ESTs; Highly similar to (define not available 4528679) [H.sapiens] |
| 100864 | 2.1 | HQ42974145 | Transcriptional Coactivator Pcl |
| 126131 | 2.3 | A020162 | claudin 3 |
| 131664 | 2.8 | AA451465 | ESTs |
| 102279 | 3.1 | D42084 | Human mRNA for KIAA0094 gene; partial cds |
| 134405 | 1.8 | J04177 | collagen; type XI; alpha 1 |
| 130287 | 2.6 | AA113149 | tumor suppressing subtransferable candidate 3 |
| 108628 | 2.1 | AA131584 | ESTs; Weakly similar to coded for by C. elegans cDNA cm16R [C.elegans] |
| 131289 | 2.2 | AA485667 | ESTs |
| 109141 | 4.2 | AA176428 | ESTs |
| 119307 | 2.5 | T32108 | ESTs |
| 134319 | 2.1 | AA129547 | ESTs; Moderately similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens] |
| 133458 | 5.0 | M18726 | non-specific cross reacting antigen |
| 118732 | 2.3 | F13779 | ESTs; Weakly similar to [H] ALU SUBFAMILY J WARNING ENTRY [H] [H.sapiens] |
| 115239 | 3.0 | AA278650 | ESTs |

CGAB

FIGURE 13B

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| Code | PRIMER KEY | Seq. Length | Accession | Complete Title |
|------|------------|-------------|-----------|--|
| CZA8 | 111929 | 3.7 | R46057 | prominin (mouse)Hike 1 |
| BCX2 | 128790 | 4.0 | AA291725 | secreted frizzled-related protein 4 |
| CBC2 | 101809 | 5.7 | M56849 | Homo sapiens connexin 26 (GJB2) mRNA, complete cds |
| CBC1 | 100385 | 4.8 | D78611 | mesoderm specific transcript (mouse) homolog |
| CBC3 | 102618 | 2.5 | U85932 | extracellular matrix protein 1 |
| CJA8 | 115697 | 8.1 | AA411502 | ESTs: Weakly similar to airway trypsin-like protease [H.sapiens] |
| CJA9 | 116176 | 5.7 | AA463725 | ESTs: Weakly similar to KIAA0226 [H.sapiens] |
| CQA7 | 115522 | 8.1 | AA331393 | ESTs |
| BCN5 | 112244 | 3.1 | RS1309 | ESTs (now Sulfatase by in-house sequencing) |
| CQA1 | 132592 | 5.6 | AA129390 | ESTs |
| BCN7 | 117280 | 5.4 | N22107 | ESTs: Moderately similar to [H] ALU SUBFAMILY SC WARNING ENTRY III [H.sapiens] |
| CQA2 | 104660 | 6.0 | AA007150 | ESTs |

FIGURE 14

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FIGURE 15

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592 ACCATGATTACGCCAAGCTTGGCACGAGGGAGACAGCCACTTGGCCATGTACCAAAAACRAGGAGAAGGTGCAGAC
TGCCGCTGTGACCTGACTCAGAGCAGAATCATTCAGAGATAAATAAGTAATCCCACCTGAATTCAGAATCATGAAA
AGCAGGAAAGCCAGGATCTCAGAGCTACTGCANAAGTTCCTTCTCCACGAGCGAGCACCANAAGCTGAGAATGCTGTT
TCCTCAGGTAACAGAGATTCAAAAGGTACTCTCAGAAGGAAGAAATCTCTACACAGATGAGTCATCCAACTCTGAAA
AATAAAAGAACTGCAATCACTACTCCAACTTTAAGAAGCTTCATGAAGTCATTTAAGGAAATGAGTCCATTGATC
AATATATTGAGAGAAAAAGAAACATTTGAAGAACACAATTCATGAATGAACTGAAGCAGCAGCCATCAATAAGGGA
GGGCTCAGGACTCCAGTACCTCCAAAGGGAAGACTCTCTGTGGCTTCTACTCCCACAGCCAGCAGCTCCCAAGCGG
GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGTCTGAAGGGTCACTAAGCGCTCTGCTATCTCTGAGCTAAACGG
GTGTCAAGTTTTCAGCTGCTACTAAAGATAATGAGCATAGCGTCACTGACCAAGACTCCAGCCAGAAAGTCTGCACAT
GTGACCGTGTCTGGGGGCACCCMAAAGGCGAGGCTGTGCTTGGGACACAAAATTAAGACCATCACGGGGAATCTGC
TGCTGTTATTACCCCATTCAGTTGACAACTGAGGCAAGCAGACTCCAGCTCCCAATAAGAAACAGTGTTTGATCTTA
AAGCAAGTTTGTCTGTCCTCTCACTATGAACCAACAAAGGAAAGCTAAACCATGGGGCAATCTAAAGAAAATAAT
TATCTAAATCAACATGTCAACAGAAATAACTTCTACAAGAAAACCTTACAACAAACCCATCTCCAGCAAGGAAGAGCA
ACGGAGAAACCGAGCAAGAACGAAAGGAGAAGAAAGGTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG
AT 593

FIGURE 16

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MTMITPSLARGQPLCHVTKTRRRCKTVRVDPDSQQNHSEIKISNPTEFQNHKEQESQDLRATAKVSPFDEHQEAEAV
SSGNRDSKVPSEGGKSLYTDSSSKPGKNKRTAITTPNFKKLHAAHFEMESIDQYIERKKKHFEHNSMNELKQOPINKG
GVRTVPVPRGRLSVASTPISORRSGRSCGPASQSTLGLKGSLLKRSASAAKTGVRFSAATKDNEHKRSLTKTPARKSAH
VTVSGGTQKGEAVLGTHKLKITGNSAAVITPFKLTTTEATQTPVSNKKPVFDLKASLSRPLNYEPHKGKLPWQSKENN
YLNQHVNRINFYKKTYPQPHLQTKEEQRRKREQERKEKKAKVLGMRRGLILAED

FIGURE 17

Amino-CKVLG MRRGL ILAED-COOH

FIGURE 18

Acetyl-KQPHL QTKEE QRKKC-Amide

FIGURE 19

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human_CAA2  -----KKNFEEHNSMNELKQPIKNGGVRTVPVPPGRGLSVASTFISQRRS
mouse_CAA2  ARFKKMESIDENIKRKKKHLKEHSSLNEIKLDKK--GIVTPVPFPGRLSVPCTPARQQCP
          ***:*.*:****   :  * :*****.**, * :
human_CAA2  QGRSCGPASOSTLGLKSLKRSALSAAKTGVRFSAATKDNEHKESLTKTTPARKSAHVTVS
mouse_CAA2  QG-----H--S--ATKMNVRFSAATKDNEHKESLTKTTPARKSFHVTAP
          **          :  * :*****.***.
human_CAA2  GGTQKGEAVLSTHKLKTIIGNSAAVITPFKLITEATQTPVSNKKPVFDLKASLSRPLNYE
mouse_CAA2  GSASKGQAVFRTPKSKATERTSIAVITPFKLITEATQTPSSSKKPVFDLKASLSRPLNYK
          *.:*:*:* * * :  * *****.*****.***.
human_CAA2  PHKGKCLKPWGQSKENNYLNQHVNRINIFYKITYQPHLOTKEEQRKKEQERKEKKAKVLG
mouse_CAA2  PHKGKCLKPWGQAKENNSLNERVSRVTFHRKITYQPHLOTREERWKRQEQERKEKKKLE
          *****:*** **:*:*:*:*****:*** :*:***** *:
human_CAA2  MRRGLILAED-
mouse_CAA2  ARRNLGVTKAQ
          **.* :*:

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FIGURE 20

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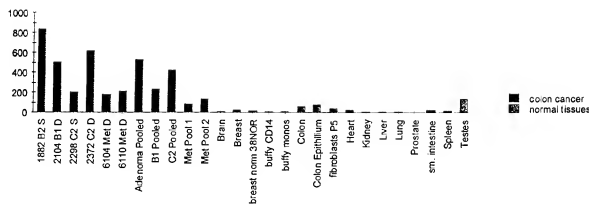


FIGURE 21

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FIGURE 22

GGTGGCCTCTGTGGCCGTCCAGGCTAGCGCGCGGCCGCAAGCGCGGGGAAGAAAGACTCTCTCACTTGGTCTTGGCGGTG
 TGCCACCCCGCGCGCAGGSGTGTGAGGCGGTGCTGCCGAGACGTCCGCGGGCTCTGCAGTTCGCCGGGGTGCGGC
 AGCTATGCACCCGCGGCCACCGGCCCTCTCTCGCGCGCCCGGACTGGCCGGGTGCGGAGACGCCCTCAQCCCTC
 CCTGGCCGCAACCCAGGTGGAACTGCCCGCACCGCTGTGCCCTCGGTGCCGAGGATGCTGCGCCCCGAGCCCGGAC
 GCGCGCGGGGTCCCGATGAGGGCCCCGCGCGCGCGGGGACCGGTGGCGACAGCCTTGGGCGCCACCCGAGCCGAGAG
 CCGTTTCAGGTGGACTGTGTTTCGAGAACGCGCGGCGGCCCTGCTGCGCGCGCGCGCGCGCGCGCGGAGCGCGG
 CGCTCTGCTGTGGCGCGGGCGCCAGCAGACCCCCCGGAGCGGGGAAGCCAGCGCGCAGACGCGCAGCTTAAAGGCA
 GAGGAAGCCAGCGCGCTTCCGCGTGAACCTTCGTGGACCCAGCTGCCCTCTGCTCGCGGTGAAGACAGCCTGTGAGTGC
 TGCCGGGTCTGAGTGCAGCGGCCCAACGTGAGCTTCAGAACCGCGGGGACACGGTGTGAGGAGAGGGCAGCAGCCTGC
 ACTCGCGCGCGCGCGCGCGCAGTGGGCACCAACAGCACTACTATTATGATACCCACACCAACACTACTACTCTGCGCAC
 TTGCGGCACAAACCACTGAGCGCTGTGCCAGGATCGATCACTACCGGCACACAGCGCGCAGCTGGGCGAGAGCTGTCT
 CGCGCTAGCCTGGCGGAGCTCCAGCAGAGCTGGAAAGAACCTTTTGAAGTAGGCTTTGCAAAATGGGGAAGAGTA
 CTCCAACAGAGATGCTGTGGTCACTGATCTAGTCAGAAAGTAAAGGAGTCGTGAAGTTTGGCTGGATCAAGGGTGTATTA
 GTACGTTGATGTTAAACATTTGGGTTGTGATGCTTTTCATTAGATTGTCATGGATTGGGGTCAAGCTGGAATAGGTC
 ATCACTCCTTGTAATAATGATGGCCACTGTTGTGCAAACTATCAGAGATTGTCATCTTCAGCAATAGCAACTAATGGAT
 TTGTAAAGAGGAGGAGCATATTATTTAAATCTAGAACTCTAGGCGCAGAAATTTGGTGGTCAATTTGGTCTTAATCTTC
 GCCTTTGCCAACCGCTGTGCACTGTGATGATGCTGGTGGATTTCAGAAACCGTGGTGGAGTTGCTTAAGGAACATTC
 CATACCTTATGATAGATGAATCAATGATATCCGAATATTGGAGCCATTACAGTCGTGATTTCTTTAGTATCTCATAGT
 CTGGAATGGAGTGGGAAGCCAAAGCTCAGATTGCTTTTGGTGTACTCTACTCTCTGATTTGGTGAATTCGTCATAGGA
 ACATTTATCCCACTGGAGACGAAGAAAGCCAAAGGGTGTTTTGGTATTAATCTGAAATATTAAGGAAGTTTGGCC
 CGATTTTCGAGGAAGAGACTCTTTCTTGTATTGGCACTTTTCTCTGCGAACTGGATTTCTGGCTGGAGCAAA
 ATATCTCAAGTGTATCTGACAGTCTCTCAGTCAGCCATACCCAAAGGAACAACCTCTAGCCATTTTAATTACTAATTTGGT
 TAACATAGGAATTCAGTATCTGTAGGTTCTGTGTGTTTCGAGATGCACTCGGAACCGCTTAATGACACTATCGTAACAGA
 GCTAACAACTGTACTCTGCGAGCTCGAAATTAACCTTTGATTTTCACTCTGTGAAGACAGCTCTGTGCTCATGGCC
 TAATGAACAACCTCCAGGATATGATATGGTGCAGGATTACACCACTAATTTCTGCAAGTATATTTCAGCCACTCT
 TCTTCAGCAATTAGCATCCCTATGATGATGCTCCCAAAATATTTCAAGCTCTATGTAAGGACAACTATCCAGCCAGTTTCCA
 GATGTTTGTCTAAAGGTTATGGGAAAAATAATGAACCTCTCTCGGGCTACATCTTAACTTCTTAATTTGCACTTGGATTCA
 TCTTAATTTGCTGAACGTAATGTTATGCAACCAATTAATCAAACTCTCTCTTGCATCATATGATGATGATCAATTTTCCA
 GTATTTCACTGCATCACTCTGMAAATCTCCAGGATGGCGCTCTGCAITCAAATCAACAACATGGGATCACTCTCTTGG
 AGCAATTTCTTGGTGCATAGTAATGTTCTGTCATTAATCTGGTGGGTGCAATGCTAACATATGTGATGCTCTTGGGCTGT
 ATATTTATGTTTCACTACAAAAGACAGATGTGAATTTGGGGATCTCTACACAAGCCCTGACTTACCTGAATGCACTCGAG
 CATTCATTTGCTCTTCGAGTGGGAAGACACAGTGAAAACTTTAGCGCACAGTCTCTGTTATGACAGGTGCTGCCAAA
 CTCACGCTCCAGCTTTACTTTCATCTTGTTCATGATTTACAAAAAATGTTGGTGTGATGATCTGTGGCCATGTACATAT
 GTCTCTGAAGACAGCCCATGAAGAGATGTCCTATCGATCAAGCCAAATATCAGCGATGGCTTATTAAGAACAAATGAAG
 GCATTTTATGCTCCAGTACATCGCAGTACTTGAAGAGAGTGCACAGTATTTGATGCAAGCTCGTGTCTTGGTCTGT
 GAAGCCAAACACACTTTGCTTGGATTAAAGAAAGATTGGTTCGAAGCAGATGAGGAGATGOGATATGATATTAATAT
 TATTTCATGATGCTTTGACATACATATGAGGATAGTGGTTATTGCGCTTAAAGAAAGGTCTGGATATATCTCACTTCAA
 GGACAGAAGAATATTTGCTCATCAAGAGAAATCTCTGCGCACCAAGGATGTGGTATGATAGTGGGATATAGTAAAAA
 GTCCGATTAGATATCTTCAAAACCACTCAGTGAAGAACCAATTAACACAAAGTTGAGGAAGAGGATGGCAGACTGCAAA
 CTCAAACCTTTGAAAAAAGAACTTCAAGGCCCTATTGTGCTTTAAATGATGACGCAAAAGCTTCTTGAAGCTAGT
 ACACAGTTTCAGAAAAAACAGGAAGAATACTATTGATGCTGGTGGCTTTTGTATGAGAGGTTTGACCTTATTGAT
 ACCTTTACCTTCTGACGACCAAGAAAAATGGAAGACTGTAAAGTACAGATATTCATGTTGGGAAGATTAACAGATTAAG
 ACCATGACCGGAGAGGCTGCTGCTTTGCTTAGCAAGTTCCGAGTAGACTTTCTGATATCATGCTGTCTAGGAGATGAT
 AATACCAACCAAGAAAGAAATAATATAGCTTTTGAAGAAATCAATGAGCCATACAGACTGATAGGATGATTAAGA
 GCAAGATATTGCAATATAATGAAGAGATGAACCATGCGGAATAACAGATAATGAGCTTGAACCTTATAGACCAAGA
 CACACCGCAGATCAGGTTAAATGAGTTATTAAGGAACATCAAGAGCTCAATATTAATGTCATGAGTCTCCAGCT
 CGCGAAAGAGTCTGTGCTAGTGCTCTCTCATAGCGATGTTAGAAGCTTATCAAGGACTACCAACCACTCTCTCT
 AGTTGTGGGATGATCAGAGTGTCTTACCTTCTATTCATTAAGTTCTATACAGTGGAGCAGCCCTCCAGAAATGGTACT
 TCAGTGGCTAGTGTATGATGCTGAATCTTCAATGACACATTAACATCAAAATGGCGAATGGTGAATCTTCTTGTGAGAT
 TCTAATTAATTTGAAGACACACAGGAAGCTTGTCCATGATATAACGTGATGGAGACTTCGGTTTATGTCAATCCATAT
 CTCAACTTAATGGTATTTCTCTCTGTGTAAGTGAAGTTTGTGAGAGTATGTTTCTTGTACTTGAATAGCATATAA
 AGCGTGTTAACTTTTTGG

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FIGURE 23

ATGGAGCGCGCGCCACAGCGCGCCCTCCTCGGCGCGCCCGGGACTGGCGGGGTTCGGGGAGACGCGCTCAGCGCGCTCGGCT
GGCCCGACGCGAGGTTGGAACTGCCCGGCACGGCTGTGCCCTCGGTGCGGAGGATGCTGCGCCCGCGAGCGGGGACGGCG
GCGGGGTTCGCGATGAGGCGCCCGCGCGCGCGGGGACGGGCTGGGACAGCCCTTGGGGCCACCCGAGCCACAGCGCGT
TTCAGGTGAGACTGGTTCCGAGAGACGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGGACGCGCGCGCGG
TGGTCTCGGGCGGGGCGCCAAAGCAGACCCCCGCGGACGCGGGAAGCGCGCGAGAGCGGACGACTAAAGGCGAGCGG
AAGCCAAAGGCGCGCTTCGCGTGAACTTCGTGGACCGAGCTGCCCTCTCGCTCGCTGGAAGACAGCTGTTCAGATGCTGCC
AGGGTCGGAGTCGACGGGCGCCAACTGAGCTTCAGAAACGCGGGGACACGCTGCTGAGCGAGGCGAGCGAGCTGCACTC
CGGCGCGCGCGCGCGCGCAGTGGGACCCAGCAGCACTACTATTATGATACCCACACCACTACTACTCTGCGACCTTCG
GCCAACACACATGGACGCTGTGCCAGGATCGATCACTACCGGCACACAGCGCGCGAGCTGGGGGAGAGGCTGCTCGCG
CCTAGCCTGGCGGAGCTCCACGACGAGCTGGAAAAGGAACCTTTTGAAGA TG9CTTTGCAAATGGGGAAGAAATGACTCC
AACAGAGATGCTGTGTCAGCTATACGTCAGAAAGTAAAGGAGTGTGAAGTTTGGCTGGATCAAGGTTGATAGGCTATCA
GTTGATGTTTAAACATTTGGGGTGTGATGCTTTTCATTAGATTGTCATGGATTGTGGGTCAAGCTGGAAATAGGCTATCA
GTCTTTGTAATATGATGGCCACTGTGTGTCACAACTATCACAGGATTGTCTACTCAGCAATAGCACTAATGGAATGT
AAGAGGAGGAGGAGCATATTTTAAATCTAGAAAGTCTAGGGGCGAGAATTTGGTGGTGCAATTTGGTCTAATCTTCGCTC
TTGCCAACGCTGTTGCAGTGTCTATGTATGTGGTGGATTGTCAGAAACCGGTGGTGGAGTGTCTTAAGGAACATTCAT
CTTATGATAGATGAATCAATGATATCCGAATTTATGGAGCAATTACAGTGTGATTCTTTTAGTATCTCAGATGCTGG
AATGGAGTGGGAAGCAAAAGCTCAGATTGTTCTTTTGGTGTACTCTCTTGTCTATTGGTGATTTGCTATAGGAACAT
TTATCCCATGGAGAGCAAGAAGCCAAAAGGTTTTTGGTTATAAATCTGAATATTTAATAGAACCTTTGGGCGCGAT
TTTCGAGAGGAAGAGACTTTCTTTCTGTATTTGCCATCTTTTTCCTGCTGCAACTGGTATTTGCTGGAGCAAAAT
CTCAGGTGATCTTCGAGATCTCAGTCAGCCATACCCAAAGGAACACTCTAGCCATTTAATTACTACTATTTGGTTACG
TAGGAATTTGCAATATCTGTAGTTCTGTGTGTTGTCGAGATGCCACTGGAAACGTTAATGACACTATCGTAACGAGCTA
ACAACTGTACTCTCGAGCCTGCAAAATTAACCTTTGATTTTTCATCTTGTGAAGACAGTCTGTGTCTATGGCCTAAT
GAACAACTTCCAGGTAATGATATGGTGTGAGGATTACACCACTAATTTCTGCAGGTATATTTTCAGCCACTCTTTCT
CAGCATTAGCATCCCTATGTAGTGTCTCCCAAAATATTTACGGCTCTATGTAAAGAACACTATCCAGCAGTTTCAGAGT
TTTGTAAAGGTTATGGGAAAAAATATGAACCTCTTGTGGCTACATCTTAACATCTTTAATGCACTTGGATTCATCTT
AATGCTGAATGATGTTATGTCACCAATATCTCAAACTTCTTCTTGCATCATATGCAATGATCAATTTTCAGTAT
TTCAGTACTCAGTCTGCAAAATCTCCAGGATGGCGTCTGCACTCAAACTACAACAGTGTGATATCACTTCTGGAGCA
ATTTCTTGTGTCATAGTAATGTTGTCATTAACTGGTGGGTCGATGTCATCAATATGTGATGTCCTTGGGCTGTATAT
TTATGTTACTCAAAAAGACAGATGTGAATTTGGGATCTCTACACAAGCCCTGACTTACCTGAATGCACTCGAGCAT
CAATCTGCTCTTTCGAGTGGGAAGCACACGTAAGAACTTTAGGCCACAGTGTCTTGTATGACAGGTTGCTCAAACTCA
CGTCCAGCTTTACTTCATCTTTCATGATTTCAAAAAGTGTGGTTGATGATGCTGGGCGCTGTACATATGGGTC
TCGAAGACAGCCCTGAAGAGATGTCCATGCACTAAGCCAAATATCAGCGATGGCTATTAAGAACAAATGAAGGCAT
TTTATGCTCCAGTACATGCAATGATCTGAGAGAAAGGTGCAAGTATTTGATGAGCGCTGCGGATATGATGAAG
CCAAACACACTTCTGCTTGGATTTAAAGAAAGATTGGTGCAGAGCAGATGAGGATGTGGATATGTATATAAATCTTAT
TCATGATGCTTTTGAATACAAATATGGAGTAGTGTTATTCGCTCAAAAAGAGGTCTGGAATATCTCACTCTTCAAGGAC
AAGAAGAAATATTGTGATACCAAGAGAAATCTCCTGCGCAAGGATGTGGTATGATGATGGGAATATGATGAAGAACTCC
GATTTAGATCTTCCAAACCACTCAGTGAAGAAACCAATTACACAAAGTTGAGGAAGAGGATGGCAAGCTGCAACTCA
ACCATCTTTGAAAAGAAATCCAAAGGCCCTATTTGCTCTTAAATGTAGCTGACCAAAAGCTTCTTGAAGCTGTACAC
AGTTTTCAGAAAAACAAAGAAAGAAATCTATTGATGCTGTGGTGGCTTTTGAATGAGGAGTTGACCTTATGATACCT
TACCTTCTGAGACCAAGAAAAATGAAAAGACTGTAAAGTCACTGAGTATTCATTTGGTGGAAAGATAACAGCAATGACCA
TGACCGGAGAGCGATGGCTATTTGCTTAGCAAGTTCCGGAATAGACTTTTCTGATATCATGTTCTAGGAGATATCAAT
CAACCAACAAAGAAAGAAATATATGAGCTTTTGAAGAAATCATTGAGCCATACAGACTACGAAGATGATGAAGAGCA
GATATTCCAGATTAATGAAGAAGATGAACCATGGCGAATACAGATATAGAGCTTTGAACCTTATGAAGCAAGACATA
CCGCGAGTCCAGTTAAATGAGTTATTAAGGAACATTCAGACAGCTAATATTGTCATGAGTCTCCAGTGTGAC
GAAAAGGTGCTGCTGCTAGTCTCTTACATGGCATGGTATGAAGCTCTATCTAAGGACCTACCCACCAATCTCTAGTGT
CGTGGGAATCATCAGAGTGTCTTACCTTCTATTCAIAA

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MEPRPTAPSSGAPGLAGVGETFSAAALAAARVELPGTAVPSVPEDAAPASRDQGGVRDEGPAAAGDGLGRPLGPTFSSOR
 FOVDLVSENAGRPAAAAAAAAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSSEAKGRFVRNVDPDAASSSAEDSLSDAA
 GVGVDGPNVSPQNGGDTVLSEGSLLHSGGGGSGHHQHYYDDTHNTYLYLRTFGHNTMDAVPRIDHYRHTAAQLGEKLLR
 PSLAELHDELEKEPFEDGFANGEESTPTRDAVVITYABSKGVVKGWIKGVLVRCMLNIMGVMLFIELSWIVGCAQIGLS
VLVIMMATVTTTTGLSTSAIATNGFVRGGGAYLISRSLOPEEGGAIGLIFAFANAVAVAMVYVVGFAETVVELLKEHSI
 LMIDEINDIRIIGAITVVILLGISVAGMEWEAKAOIVLIVILLLAIGDFVIGTFIPLSEKKPKGFFGYKSEIFNENFGPD
 FREETEFSSVFAIFFPAATGILAGNISGDLADPOSAIPKQTLILAILITTVVYVIAVSVSGCVVRDATGNVNDTIVTEL
 TNCTSAACKLNFDFFSCSSCPSCSYGLMNNFQVMSMVSQGTPLISAGIFSATLSSALASLVSA PKI FOALCKDNIYPAPQM
 FAKGYGKNNPLRGYILTELIALGFIILAEINVIAPILISNEFLASVALINFSVFHASLAKSPGWRPAFKYYNMWISILGA
ILCCIVMEVINWMAALLTVIVVLGLGIYYTYKKPDVNWGSSTQALTYLNAHQHSIRLSGVEDHIVGNFRPQCLVMTGAPNS
 RPALLHLVHDFTKIVGLMICGHVIMGPFRQAMKEMSIDQAKYQRLIKNKMKAFAYPVHADDLREGAQYLMQAAGLGRMK
 PNTLVLGFKKDWLQADMRDVMYINLPHDAFDIQYGVVVIRLKEGLDISHLQCGEELLSSQEKSPGTDVVSVEYSKKS
 DLDTSKPLSEKPIETHKVEEDGKTATQPLLKESKGPVPLNVADOKLEASTOFQKQGGKNTIDVWMLFDDGGDLTLIP
 YLLTTKKMKDCIKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTPKKKENI IAFEEI IEPYRLHEDDKEQ
 DIADKMKEDPWRITDNELELYKTKTYRQIRLNELLKEHSSSTANIIVMSLPVARKGAVSSALYMAWLEALS KDLPPILLV
 RGNHQSULTFYS

FIGURE 24

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FIGURE 25

| Peptide names | Solubility | |
|---------------|-------------------------------|------------------------------------|
| CAA9p1 | 1mg/1ml H ₂ O | H-CDPAASSSSAEDSLSD-NH ₂ |
| CAA9p2 | 1mg/1ml H ₂ O | Ac-KKSDLDTSKTLSEKC-NH ₂ |
| CAA9p3 | 1mg/1ml H ₂ O | Ac-PLLKESKGIIVPLC-NH ₂ |
| CAA9p4 | min.amt DMSO/H ₂ O | Ac-ENSLIMIDEIC-NH ₂ |
| CAA9p4MAPS | 1mg/ml buffer pH7.5 | Ac-ENSLIMIDEIC-on 8-Branch Maps |
| CAA9p5 | 1mg/1ml H ₂ O | Ac-DFREEETC-NH ₂ |
| CAA9p5MAPS | 1mg/1ml H ₂ O | Ac-DFREEETC-on 8-Branch Maps |

FIGURE 26



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FIGURE 27

GGCACGAGGAGAACTTAAAGAAATTCAGATATGTGAAGTTGATTTCC⁵⁴³⁵GAAACCTCGTCA
TCTCTGATGACAGTGTGTGACAGCTTTCCTCTGATAATTTTGCAAAACACGAGGCTCGACGTCA
GTTCCGGGAAGGCTGTAGGACCCGACGCCAGTGCAGGCCTCTGGAACCTCTCAGGGTGGCGAT
GAAGTTTCCAGCGCGGAGTACCAGGGGAGCAACCAACAAAAAGCAGAGTCCCGCCAGCCCT
CAGAGAAATCTGTGACTGATTCCAACCTCGATTACAGAAAGATGAAAGTGGAAATGAATTTTITGG
AGAAAAAGGGCTTTAAATATAAAGCAAAACAAAGCAATGCTTGCAAAACATGCTGTGAAATTA
GAAAGCTTCCCTGGCTCGTTCCTGTGGAAGACATCCCTCCAGGCTCCGACTCACAATCAAGG
AGACCGCAAGAGCGCTACATTCCTCCGGGTGTGTCTCCAGGAGAAACCTGGAACGGAGAGCTCG
TCTCTTACCAGGTCAGGGTCCCGGATCTCCGGTCCCTTGACGCTCTACCCATGGAGGAGGA
GGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGCCGTGGATGGCTACATGAAT
GAAAGTAGACCTGCCAGAACCCGTCGCTNCAGATCATCCGTGACCTTCGCGATATAATTCGC
CCAGTGGAGAGAAATACAGAAAGGAGGAGGTGGAGAACGCTTCGACGAATTTTCGAAAGAGA
AGATTATAACCGTCTACTGGGTTCTACTTGTATCAATGCCGTGAGAAAGACTATTGATACCAA
AACAACATGCGAGAAACCCAGACTGCTGGGGCGTTCGAGGCCAGTTCTGTGGCCCTCGCCTTCG
AAACCGTTATGGTGAAGAGGTGAGGATGCTCTGTGATCCGAAGTGGCATTGCCCCGCTTG
TCGAGGAATCTGCAACTGCAGTTTCTGCCGGCAGCGAGATGGACGGTGTGGCACTGGGGTCTCT
TGTGTATT⁵⁴³⁶CCAAATATCATGGCTTTGGGAAATGTGCATGCCCTACTTGAAAGCTGAAACA
GGAAATTTGAAATGCAAGCATAAATATCTGGAAAAATTTGCTGCCCTGCTTCTACTTCTCAATCTT
TCTTGTAAAAATTTCCAATTTTTCACGTGAAACCTGAGTTAAAAATCTGTGATGATCAGCGCTGT
TTCATAAGAAAATCTCAATCAAGTTAMTCTTAGCAGACATGTGTTTCTGGCCACTCAGCAAGG
TATATTGCTAGTTACACTTTGCCCTCTGCAAGTTTCTCTCTGCTCCCAACCCCACTCTCATAGG
ATCCCCCTCTATT⁵⁴³⁷TTCCATTGCTCCCTCTCCCAACCCGCTTAAAGTTTCTGTAATTTTCTTTTA
AAWTTACAGTTTAAAGGAAAAGCCATATTTTATTTTACCTGGGTGTGGGAAATAGCCCCCTCAT
AAAAACCTTAAGCACTTGGAAACACAATAATAGTATTAACCTTAAGTATCTATTGAAATTTCA
GAGAAGAGCGCTTCTAATCTGTTTACACAAAAACGAGTATGATTAGCATTCATACTAGTTGAA
ATTTTAA TAGAATCAAGGCACAAAAGTCTTAAAAACCATGTGGAAAAATAGGTAATTATKGC
ARATTGAGGTGTCYCYCAATCCCAAGWTGKSGCTTATGKTACMARKKGTGTCMCAAGTTRAG
ACYTAAATTTCYCTAATTTCTTCYGGCCGAAGGKWAAGKGGKGGTCCRGCTTACMCGATCAT
AATTCMAAGGKGGKGGSCAATGTAAATTTCAATTTAAAAATATKRWGGAAGAGCYATCTGG
AGATTAWGAGTAAAGCTGATTGTAATTTTCAGTATAAAACCTTAGTATAATTGTAGTTTGCAA
GKTATTTTCAGTTTACATGTAAAGGKATTCMAATATAATCTTGGCAATTTTGKATGGAAACT
TGATATTAATAAACTAGTCTGTGGKTCCTTTCAGTTTCTTGTAATTTTATAAACCGGACAAAG
GTTCAAGTTTATAGTTTAAAGCACTTTTATAACAATGATAAGTGCTTTTGGAGATGTAACCTTT
TAGCATGTTGTAACTGACATCTCTGCCAGTCTAGTTTCTGGCAGGTTTCTGTGTGAGTAT
TCCCTCTCTCTTTCATTAATCAAGGTTTGGTAGAGGTGGAAATCAAGGCTTTGTGATGTC
CAATTTACTTGCATATGTAAACCAATTCGTGCCCCATTCATGTTTGTATGCATTAATTGGAC
CTGTAATCGATAAGTGTAAATACAGCTTTTGTATCTGTAATGCTTTTATACAAAAGTTTATT
TTAATAATAAAATGTTTGTCTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
CCWTTATGTGAGKSWTAAATTTAGCTTGGCACTGGCCGCTCGTTTACAAACGTCGTGACTGGGA
AAACCCCTGGCTTTACCAACTTAATCGCTTGCAGCACATCCCTCTTTCGCCAGCTGGCGTAA
TAGCGAAGAGGGCCGCAACCGATCGCCCTTCCCAACAGTTTGGCAGCCTGAATGGCGAATGGG
ACGCGCCCTGTAGCGGGCGCATTAAGCGCGCGGGTGGTGGTTACGCGACGCTGACCGCTA
CACTTGCCAGCGCCTTAGCGCCGCTCTCTTTCGCTTCTCTCTCTCTCTCGCMCGTTCCGCGG
CTTTCGCCKAGCTNTAAATCGGGG

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One position equals 20 bases

■ if more than 2 bases disagree with consensus sequence

■ if more than 10 positions are unknown

■ if more than 10 positions are gap characters

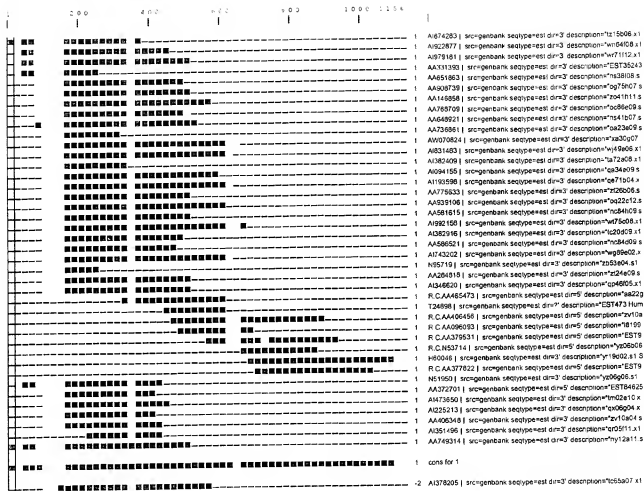


FIGURE 28A

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| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 2 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 3 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 4 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 5 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | | | | | | | | | | | | | | | | | | | |

cong. for 1

AJ378205 | src=genbank seqtype=est dir=3' description="ic65a07 x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE 2069460 3', mR" src=gbest26/6489

FIGURE 28B

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MTSSSSDDG CDSFASDNFA NTRLQSVREG CRTSQCRRHS GFLRVAMKEF
ARSTRGATNK KAFSSROPSFN SVTDGNSDSE DESCHNFLEK RALNIKQNKKA
MLAKLMSELE SFPGGFGRRH FLPGSDSQSR RPRRRTPFGV ASRRNPERRA
RELTRRSRI LGSLDALPME EEEEEDKYML VRKKRTVDGY MNEDDLPRTR
RYRSSVTLPH IIRPVVEIQK ERSWRISAAI LEEKIITVHW ALLVINAVRR
LLIPKQTAET CTAGAFEASS VAPAFETVMV KRSGMLCWIR TGIARLVEES
ATAVSGAGEM DGVRLGSLCI

FIGURE 29

WO 00/55633

PCT/US00/07044

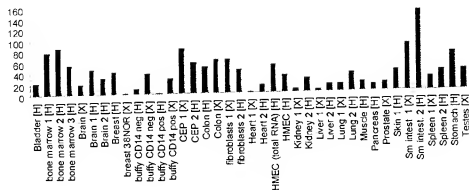


FIGURE 30A

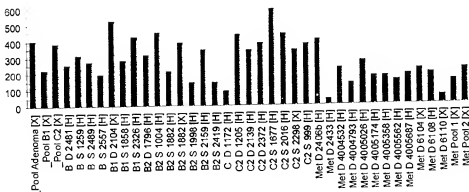


FIGURE 30B

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WO 00/55633

PCT/US00/07044

ACTCACTATNNGGCGAATGGGCCCTCTNNATGCATGCTCGAGCGCCGCCAGTGTGATGGATA
TCTGCAGAAATTCGCCCTTAAAGCAGTGGTAACAACGACAGAGTACGCGGGGGAGACCGGAGGG
CAGAAAGCAGAGTCCAGGCTTAGAGTGCAGTTCCTCGCTTACCTGTGCAGTCTAATTTTGAGC
TGCCCTCTTTGTAGTCTTAAAGGCGAGGAGCTTCGTGTTGTGGGTCTGCTAACCCGTACGTTTCC
GTGGGCAAGTCGTGTGTAATCCTCGCCCTGCTCAGCTCCAAACACGCTTCTACACTGATAAC
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCTCTGAAATTCGCGACCTTA
GTAAACATCATCAATAAACTACTAAAGGACAAAATGAGTTCACAAACATGTGGAGTTTGATT
TCCTTATTAAGGGCCAGTTTCTGCGAATGCCCTTGGACAAACACATGGAAATGGAGAACATCT
CATCAGAAAGAGTTGTGGAAATAGAATACGTGGAGAAATATCTGCACCCAGCCAGAGCA
TGCATGTTCCATGATGACTGGATCAGTTCATTAAGGGGCGAGGAAATGGATCTTGAGTGT
TCTTATGATAAGACTTCTCGGATCTGGTCTTGGAAAGGAAAGTCAATAATGACAATGTGGGA
CATACGGATGTTGTAAGATGTGGCCTGGGTGAAAAAGATAGTTTGTCTGCTTATTATTG
AGTGCTTCTATGGATCAGACTATTCTTATGGGAGTGGAAATGTAGAGAGAAACAAAGTGA
AGCCCTCACTGCTGTAGAGGTCTATGCTGGAAGTGTAGATTCTATAGCTGTGTGCTCAGG
AACTAAATTTTGCAGTGGCTCCTGGGATAAGATGCTAAAGATCTGGTCTACAGTCCCTACAGA
TGAAGAAAGATGAAATGGAGGAGTCCACAAATCGACCAAGAAAGAAACAGAAAGACAGAAAG
TGGGACTAACAGGACTCCCATAGTGACCTCTCTGGGCCATATGAGAGGAGTTCCTCAGT
CTGTGGTCAAGTGTGAAGAAATCTCAGTGCTCTCTGGGACCATACAATTAGAGTGTGGGT
GTTGAGTCTGGCAGCTTAAAGTCAACTTTGACAGGAAATAAAGTGTCTAATTGATTTCTATT
CTCCACTTTGTAACGTTTATGCACTTGGAGCAGACATAGGCATATCAGACTGTGGGATCCCC
GAACATAAAGATGGTCTTTGGGTCTGCTGCTGCTTACGTCACACTACTGGTGGGTGACATCAG
TAAATGGTCTCTACCCATGAACAGCAGCTGATTTAGAGATCTTTAGATAACATTTGTAAGC
TGTGGGATACAAGAAAGTTGTAAGGCTCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTTC
TGAGTGTAGACTGGACAGACACAGGGCTACTTCTGAGTGGAGGAGCAGACATAAATTTGAT
TCCTACAGATATTCACCTACCCTTCCCATGTTGGGCACTGAAGTGAACAATAATTTGACTA
TAGAGATTATTTCTGTAAGTGAATTTGGTAGAGAACCATGAATACATAGATGCAATGCA
GAAAGCAGCCCTTTGAAGTTTATATAATGTTTTCACCCCTTCAATAACAGCTAACGTTATCACTT
TCTTATTTGATTTATAATAAGATAGGTTGTGTTTATAAAATACAACTGTGGCATACA
TCTCTATACAACTTGAATTAACCTGAGTTTACATTCTCTTTAAARGTAAAAA
AAAAAAAA

FIGURE 31

WO 00/55633

PCT/US00/07044

One position equals 17 bases.

- if more than 1 bases disagree with consensus sequences
- if more than 8 positions are unknown
- if more than 8 positions are gap characters.

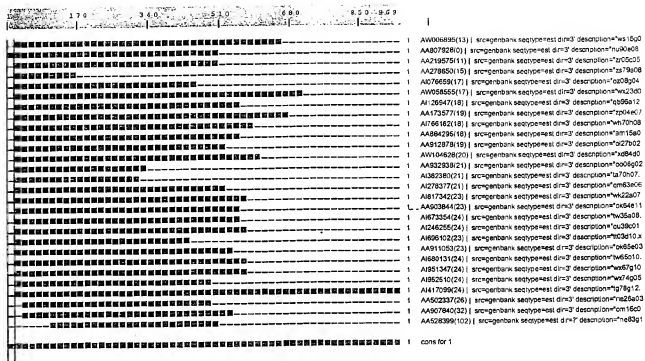


FIGURE 32A

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| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 2 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 3 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 4 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
| 5 | 1 | 2 | 3 | 4 | 5 | 6 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

const for 1

FIGURE 32B

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MAQLQTRFYTDNKKYAVDDVPFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDF
 LIKGQFLRMLDKHMEMENISSEEVVEIEYVEKYTAPOPEQCMFHDDWISSIKGA
 EEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKDSLSCLLLSASMD
 QTILLWEWNVERNKKALHCCRGHAGSVDSIAVDGSGTKFCSSGWDKMLKIWS
 TVPTDEEDEMEESTNRPRKKQKTEQLGLTRTPIVTLSGHMEAVSSVLWSDAEEIC
 SASWDHTIRVWVVEGSLKSTLTGNKVFNCSYSPLCKRLASGSTDRHRLWDP
 TKDGSLLVSLTSTHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCAPLYDL
 AAHEDKVLSDWTDGTLGLLSGGADNKLYSYRYSPTTSHVGA.

FIGURE 33

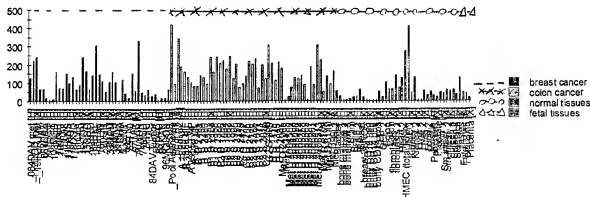


FIGURE 34

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[illegible]

FIGURE 35

[illegible]

FIGURE 36

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PCT/US00/07044

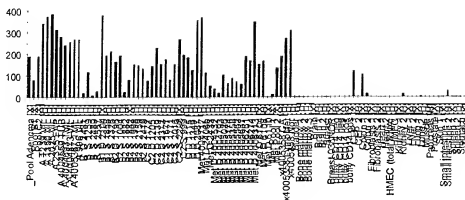


Figure 37

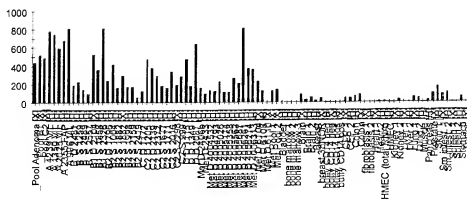


Figure 38

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AGAAATCCCTTCGRCCTCCITTCGCCGCCCGGTATTCCTGGTATATGATCCCACTCTCACTCTCAIAGGAGAC
 GATCTCGAAGTAGATCATATACACCAAGATACCGGCCCGCGAAGGAGCCGAAGCTCAAGGGTAAGACACTA
 GAAATATTACTCAGTAACCAATAATGTGGAACCTTTAAGATGGATAATAGGGCATGGACTGAGTGCTGCT
 ATCTTGAAATGTGCACAGGTACACTTACCTTTTTTTTTTTTTTTTAAAGTTTTCCCATTCAGGATAACA
 ACATTGTGATCTGTACTACAGGAACCAAAATGTCAGCGGTCAATACATGTGGCTATAAAGTACAT/AAAAATA
 TCTAACCTATTCA/ATGTGGGGTGGGTAAATACCTGCTGTGAAATAAATGTAAGAAGCTTTTCACTTAAAAAA
 AATGCAITACTTTCACCTTAACACTAGACACCCGGTCGA/AAATTTTCAAGGTTATAGTACTTATTCAACAA
 TTCTTAGAGATGCTAGCTAGTGTTCAGGCTAAAAATAGCTTTATTTATGCTGAATTGTGATTTTTTATGC
 CAAAATTTTTTACTTCTAATCATTCATGATAGCTTGG/AAATAAATAATATGCCATGGCATTTGACAGTT
 CATTAATTCCTATAAGAAATAAATTGAGTTTAGAGAGAACGGTGGTGTGAGCTGATTATTACAGTTACTG
 AANTCAAAATTTATTTGTTACATTATTCGATTGTATTTAGGTTTCCITTTACATTCTTTTATATGCA
 TTCTGACATTACATATTTTTAAGACTATGGAATTAATTTAAAGATTAAAGCTCTGGGGATGATTATCTG
 CTAAGTAACTCTGAAATGTAAATTTTGA/TAATACTGTAAIATACCTGTCACACAAATGGCTTTTCTAATG
 TTTTAACCTTGAGTATTCAGTTGCTGCTTTGTACAGAGGTTACTGCAATAAAGGAAGTGGATTCTAT/AA
 CCTAAAAA/AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 39

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CCAGTTCTACCTCAIGTTTGGAGGATCTTGCTAGCTATGSCCCTCGTACTCGGCTCCCTGTTGCTGCTGG
 GGCCTTGGCGGMACTCCITTTTCAGGAGGGCAGCCTTCATCCACAGATGCTCCTTAGGCTTGGAAATTAIGAA
 TTGCCCTGCANCAAAATTATGAGNCCCAAGACTCCCAATAAGCTGGACCCATTGGCATTCTCTTTGAACATGT
 GCATATCTTTCTATGTGGTACAGCCGCGTGATTTCCAGAGAGATACTTTGAGAAUATCTTTACCAAGAGG
 CATATGNAVCCAAATTTGATTATGCAAGCCAGAAACTGTAAATCTTAGGTCATAAGATTGTCTACTATTGAA
 CAGAGGATTAATTTATGCTGTGCTCGGCTGCTGTTTATTATTCTGATGCTCTGTGGGGTAATTTCTT
 TTGTATGTGTCGTTGCTGTAAACAAATGTGGTGGAGAAATGCACAGCAGCAGNAGGAAUATGGGCCCTTCC
 TGAAGNAATGCTTTGCAATCTCCCTGTTGSGTATTGTATAATAAAGCATTGGCATCTTCTATGGTTT
 GGGCACTATCACCAGGAAAGAACCCGATCNAAAGGATCGGAAACTGGCAGATAGCNATTTCAAGGACTT
 CGGATCTCTTTGAATGAACTCCAGAGCAATCAAAATATATATTGGCCAGTACACACTACCAAGGACA
 AGGCCCTTCCAGATCTGAACAGTATCNATTCAGTGTAGGAGCGGAAATCTTGAACAGTACAGACCCAAAC
 AATCATCCCTGTTCTTGATGAGATTAACTCCATGGCAACAGCGATCAAGGAGACNAAAGGCGTTGGAGAA
 CATGNAACAGCACTTGAAGAGCTTGACCAACAAAGTACACAGCTTAGCAGCAGTCTGACACAGCGTGAUAA
 CTAGCCTCCGCTCATCTCTCAATGACCCTCTGTGCTTGGTGCATCCATCAAGTGAACCTGCAACAGCATC
 AGATTGCTCTAAGCCAGCTGAATAGCAACCTGMACTGAGGCGAGCTTCCACCCTGATGCAAGNACTTGA
 CAACTGTAAUAACTGTTCTTAGGACAGATTGGATGGCTGGTCCCAACGGGCTATCAATCCCTTAATGATA
 TACCTGACAGAGTACNACGCCAAACACAGACTGCTGTAGCAGGATCAAAAGGCTTCTGAATCCATTTGGT
 TCAGATATCGACAGATGTAACTCAGCGCTCTTCCCTATTACAGATACTACTCAGCATTTCTGTTATGTTAA
 TAACTCATGAAAGTATCATCCNAGAAATTTACTACATTGGMAAGNATGATCATACTGGTGGCTGGGTG
 GCTGGCTCATCTGCTCTCCTGACCTCATCTGATTTTATCTACCTGGGCTTACTGTGTGCGCTGTGCG
 GGCATACAGAGGCATGCCACCCGACCCACCGAGGCTGTGCTCCMAACCCGAGGCGCTTCTCTCATGGT
 TGGAGTTGGATTAAGTTTCTCTTTTCTGGATTTGATGATCATTTGTTGTTCTTAACTTTGTCTTGGTG
 CAAATGUGGAAAACTGATCTGTGAACCTTACAAGAGCAAGNATTAATCCGGGTTTGGATACACCTTAC
 TTAATGATTAAGAGCTGGGAATACTATCTCTCGGGAAGCTATTAAATCAAAATGNAAGCTCACITTT
 TGAACAAGTTTACAGTGACTGCAAAAAAATAGAGCACTTAGCCGACTCTTCACTCGCAAGACAGCTCA
 ATATCASTGMACTCTCAACATTAAAGCATCTGGAGCATAGCAGTGAATGGUATCTGTGAAGTGA
 NAATCTTAATATTTCTGTGGTGCAGCAGGAAGAAACCTTCAGGATTTGCTGCTTTGTGGAAATAGA
 CAGAAATGAATTAAGACAGCTACTTGGCTCAGACTGGTAATCCCCGAGGAGTGAATCTTTATCATTTG
 CNATGMACTAGAGCAAGCAAGCAAGTTTGGCCCGAGGAAATTTGAGGAACCTCCCTGAAAGAGATGCA
 CAACTATTAAUAACTTCAACAGCAACGAGTCTTCTATAGAAACATCACTGAGCACTATACACCAAG
 CGTCAAGATACTTCAACGCACAGGGAATGGATTGTTGGAGNAGTAAGTATGATTTCTAGCTTCTCTGGAAT
 TTGCTCAGAACTTCACTACAAACAAATCTTCTCTGTTATTTAGGAGAACTAAGAGATATGGAGNACA
 AATNAGGATATTTGACNNTATCTGAGCTGGATCGAGTTCTCTATCTGAGAAAGTGGCATGTGCAAA
 AACTGTGGCCACCGCTAGATATCTGCTGTGATGCTTTCTGTGTAGCTACATTATCGACCCCTGMAAT
 TGTTTGGTTGGCATAGGAAAGCTACTGATTTTTACTTCCGCTCTAATTTTTGGGTAAGAACTGGCT
 AGTACATCTGTCGAATGGATTCCGAGGACGTGACGATGATGTTGAACTATACCAATGAAATATGGA
 AATGGTAATATGGTTNATATAAGATCATGTATATGGTATTCACAACTCCTGTTATGACAGGCCATCAC
 AACACTGATAGATGTTGAAACTGCTTGAGCATCAGGATCTCAAGTGGAAAGGATACAGAAATTTTG
 CTAGTTTCTGGGCTCTCAGGACTTTCCAAATCCAGAGCAACCCGAGTGCAACGTATGTACTCAGGCGG
 GCAACAGGCAACCGCACCATTTGCTCTGGGTAGTGCTTTAAGAAATGAACACATCAAGTTATAGTCCAAT
 GGTCCATCACTATTCAAGGATGACTCTCCCTCTCTCTATTTTGTGTTTACTTTTATCACTAGAT
 TCTATTTAGACACTACACATATGGGGTGTTGTTCCATTTGGATGCAATTTCTATCAAACTCTATCAAA
 TGTGATGGCTAGATTCAACATATGCCATGTGTGGAGTGTGCTGAACACACAGGATTACAGGGAAGAT
 GCATTTTGTGTACAGTAAAGCGTGATATACTTTTGTACACAGAGTTTTTAAACAAATGAGTATTA
 AGGACTTTCTCTAAATGAGCTAAATAGTCACCAATGACTCTTGGTGTGTTGAAATTAATCCATTTTC
 ACTAAAGTGTGTGAACCTACAGCATATCTTCAAGCAGAGATTTTCTATTAATACTTATCAAAAGAT
 TGGCATGTTCCACTTGGAAATGGCATGCAAAAGCCATAGAGAAACCTGGGTAACTCCATCTGACNA
 TCTCAAAAGAGAGACAGAGACTCTTGAGAGNAAATGCTGTGCTTCAAAAGTGAAGTTGTTTAAAGAGTGC
 CAATTAAGGTGACAGTTTAAACAGAGTTTCTGTGATTAAGGTAACATTAATTTGAGTGCAGCTACACA
 TGAATCTATCAGACTAGTATCAAGTTGTCTAAATGAAATAGAGAGTCCCTGTCAACTTTCTAGTACT
 TGGTGCTCGAGCATGGATCAAACTTTGAGTTTGGTCCCTTAATTTGCATGAAGCAACAGGTAATATCA
 TTTGCTCAGAGGTTTCTGTTGGATCTGTCAATTAACAAAGTACAGAAATGAAGACTGGTGGGACACA
 AATTTAGCTGTAGTGAATGGAATCCAGATGAGGCATTCGCCCCAGGCTTTTCTATGTGCAATTTGAG
 TTTCTGATCTATTAATAAAAAGAACTGG

FIGURE 40

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FIGURE 41

FIGURE 42

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CGCCAGCACACCCGCCACCTCCTCTGCGCGAGCTGCCCTCGCAAGCGCAGTCCCGCAGCGCAGCGCC
GATGTGCTGTAGCTGCTTGCCTGGCGCGGCTGCCGCTCGCGGGCTGTGGGCTGCGGGCTGCGCCCTGCTG
CTGTGCGCAGCTCTGCACCCCTTGCGGGCTCTGCGCGCGCCGGTGCTCTGCACACGCTCCGGCGGGCGGCATG
GGATTAACCGCCCGAAGTGTGCGCGGAGATCGCTCCGAGGATGACGGAGTGGTGCTCCAGGTGGGGCTG
CTGCCCTGCCCTGCTTGTGCGGTACCTGCACATCCACCCCTCAGCTCTCCCTTGCCTTCTACTCAT
GGANGCTCATCGCCAGTTTTTCACTTACACGGGACTGCGTATCTCTACCAAGACTCTGTGGGTGGGT
TGGAGCTCCAGAGATACTTGTGCTTTTACACGGTITTCACATCCAGCTACGACTGGTACAGATTTGG
TAGCTCTCGACCTTGAGGTTTATCGGGTGATTGCCCTTGATTTCTTAGGCTTGGCTTCAGTGACAAAC
CGAGACCACTCATTTTCCATATTTGAGCAGGCGCAGCATCGTGGAAAGCGCTTTTGGGCACTCTGCGGCT
CCAGACCGCAGCAATCAACCTTCTTCTCATCACTATGGAGATTTGCTCAGGAGCTTCTCTACAGG
TACAGCAGAGATCGATCTGTGCGGCATACCATAAAGAGTCTCTGTCTGTCTAAATGGAGGTATCTTTCTGT
AGCTCAGCGTCCACTCTTCTCCAAAGCTACTCMAAGATGGAGGTGTGCTGTCAACCATCTCTCACAG
ACGATGAGAACTCTTTGATTTCTCGAGGCTTCACCCGAGTCTTTGGGCCGTATACTCGGCCCTCTGAG
AGTGAAGCTGTGGGACNTGTGGCAGGGATCGGCAACATGACGGGAAGTGTGCTATTGACAGTCTCTTAC
AGTACATCAATCAGCAGGAAGAGTTCAGAAAGCGCTGGGTGGGAGCTCTTGCCTCTGTAACTATCCCCAT
TCATTTTATCTATGGGCCATTGGATCTGTAAATCCCTATCCAGAGTTTITGGAGCTGTACAGGAAAAG
CTGCCCGGCTCCAGAGTGTGATTTCTGGATGACCACTTAGCCACTATCCACAGCTAGAGGATCCCATGG
GCTTCTTAAGATGCTATATGGGCTTCATCACTCCTTCTGAGCTGGAAAGAGTAGCTTCCCTGTATTAAC
TCCCTCACTCCCTATATGTTGTGTATTCCACTTAGGAGAAATGCCAAAGAGGCTCTGGCCATCAAA
CATTAATTTCTCTACAAAGCTCCACTTACTCAATTTGGTGAACAGTGTATAGGUNGAAAGCAGCAGGAGCT
CTGACATAGGTTGACATTAATAGTCCACTCCCATTACTTTGATATCTGATCAATGTATAGACTTGGCT
TGTTTTTGTGCTATTAGGAATTTCTGATGAGCACTTACTATTCACTGATGAGAAAGAGCTCTTTTGA
TAAAGAGCTTTTAAACATTTGGACTTCTCTGAATATTAGAGTGTCTAATTTTGGGCCACGGCCC
AAGAGGAAATCTATAGTAGGAGGAGGAGAGGGGGGCTCCTTCCCTCTCTCGAATGACGTATAGGGCA
CATGCTTTTAAAGTCTTTAAGCACACAGAGCTGAGTCTCTTTGTCATACCTTTGGATTATGTGTT
TCATCAGCTGTTTTAGTTATTAACATTTTGTATAATAGATATTGGTTAAATGATACAGTATTTTAGG
TATGATTAAAGCATATGATTTACCTATACATTATATATTTTAAAGATACATAACAGCATACCTT
ACCTCTGCCAGAGTAGTGAAGCTAATTAACACGTTTGGTTCTGAATAAATGAACATAATCCAACTAT
TTCTCTAAATCAGAGCAATTAAGSACCAATAGCATCTGTGCCAGAGATGTACTGTATTAGCTGGGAAG
ACCAATTTCTAACAGCAATTAACGTTCTGAGACTCTCATACCTCAGTGGTTAGAAGCATCTCTCTTGA
CTTACTCTAGAGGGGAGGAGTTGTGTGATGCTAAGTACCATGCTGATGTGACACTGATTCCTTTATG
ATGACTGCTTAAGTCCCACTGCTGTGCCAGAGAGCTTCCAAATGTAGCTCAGTAATTCCTGTTACTT
TAGAGACGGAAAGTTCCAGAACTTTAAGACAAACTCTGAAGACCTATGAGCAATGTGTCTGATTA
CTTTTATTAAAGCCACATTTCAATGCTTAGTCAAGCAGGATTTAAGTGATTTAATAATTCGT
TTTTTAATTAAGCACTTCAAGATATACACTTGAACCTGGAATAGTGTTATTCTTATTATAAA
AATGATTTGTACAAAANAAAAAGC

FIGURE 43

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CTCTGAGTGTCCAGTGGTCAGTTGCCCCAGGAATGSGGAGCCACAGCCAGAGCAGCCTTGGTCTTGACCTAT
 TTGGCTGTGCTGCTGCTCTGAGGGAGGCTTCACGGCTACAGGACAGAGGCAGC1GAGGCCAGAGC
 ACTTTCAGAGAGTTTGGCTAGCAGCTCCCCCTCCCCACCCCTATCCCGAAGCCTCCCCATGGATCACCC
 TGACTCTCTCAGCATGGCCCTCCCTTGAGGGACAGAGTCAAGTGCAGCCCTCTCTCTCAGAGGGCC
 AGCCCTCTCCACAGGAAAGCTGCTTACCTGCCCACTCCCTGCTGAAAGGAGTGGGTCCCCCTCTCC
 CTGAGGAAGCTTCCCCCTCCAAAGAGCTGCCCTCTCTCCAGCACCCCAATGACAGAGGAGGAAC
 CCGAGCTCCATTGGGACCCAGGCCATCCAGAACCTGAGTCC1GGATGCAGCCACAGACTGCCACAG
 GACCGTCCCAAGGCGGCTGGGGCCACCGGCTGGATGGCTCCCCCTGGGCGCCTCTCTCAGACATC
 TGAACCAATCTGGCTTCTAACTGTCAGCATGGTGTATATGGTCCCTGGAACCTACCAAGCTCCAGCTA
 CTCCACCTCACTCCCCAGGGTCAGACCTCAATTTCTGGAGATTGATATCCCGCTGCCTGCAT/GC
 CCGACCCACACAAACGCTAGAGTGTGCCAACTTGTGGGAGGAAGCAATGAGCCGATCTGTGAGS
 CCGAGTTCTCGGTCAAGACCCGACCCCACTGGTGTGTGACCGGGCAGGGGAGGCTCGGTCTCTCTGT
 CCAGGAGGAAGTCCCCAGCCACACTACCACTCCGGGCTCGCCAGCCATCAGCTGATATTTCTCTG
 GGTCTTGAGCTCTCTTCCCTCTGGGCTGCCACATTSAGACAATATCAAGAACATCTGCCACCTGAGGC
 CTTCCGCTCTGTGCCACGCACTGCCAGCTACTGACCCCTACAAAGGGAGCTGTGGCACTGATCA
 GTTGAAGAGGAGTCCAGCGCTGTGCGGCGAGGGAACTACACCTGTACATGGAAGCTGTGGAG
 GATACCTTGAACAATACTGTGACCGGAGTATGCTGTGAAGACCCACCACTTGTGTGCTGCCGCC
 CTCACAGCCCTACTCGGATGAGTCTTGTGCGGCTCTTACCCCACTATGACCGGCACTT
 GACATTAACATATCTCTGGCTGATCCACACACTGAGGCGCCTCTGTGAAGCAAGAGTCTCACC
 AAGCCTGCTGTCCAGAGGAGGAGAAATTAACCTCATCAATGATCTGTGTGCTCCGCAATTTCCAGAC
 CCGAGACCTCGCTCTGTGCTTACTGAGTCTGGGATGAACAGCTCACTGCTTCACTATCACTAT
 CTGAGGACCTGGCTAGTGTCTGAGACACTGAGAGCCCAAGGSCAGGGGAGCAGGCTCACTG
 GAGGACAAATATCACTCCTCTGAGCCCAAGGAAGAAAGTCACTCAGCCAGAGCCTAGAGGGTCA
 ATG

FIGURE 44

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ATCTCATTATYAGGGCTCGAGCGGCCGCCCGGGCAGGIGGCCACCCACCATCATCTAAAGAAAGTAACTTGG
CMAATGACATCGAGGTTCTCAAGGCAATAAATCCAGAAUATCTTCAAGGACCCCTATCTGCAAGATGT
CTGMAATACCTCIGAGATATAGAGATTAATATTCMAACGAGTAACCTAATTCAGAGTACTCCAGAAATCAGGA
GACGAGACATTTTGTGAGTTTGTCAACATTTGGACCAATACAACTCAAGTATTCTTGCTGTGCTCTGGTIT
TGGGTCCTCGGSCAGAGAAATGCTGGGSAAGCCTCTCTCGAGCTTCAGATCCCCGAGGTCAGAGGACGG
ATACAGGAGAGACMAAAACATCCGACCCAACTATTTCTGTGCTTACCGATGATCAAGATGTGGAGGAT
GGGTCCTCGCAATCATGACMAACAGAGAAAGATTATGGAACTAGGGGGGCCACCTTCATCAATGCGCT
TTGTGACTACCAUATGTGCTGCCGTCCAGGTCCTCATGCTCACCGGAAATGATGTCCACAATCACAAAT
CTCTACACCAACACAGAACTGCTCTTCCCCCTCGTGGCAGGCCATGCAATGAGCCTCGGACTTTTGTGT
ATATCTTACCACTACCTGCTGCTACAGAACAGCCTTTTGGAAUATACCTCAATGAATAATAATGGCACTACA
TCCGCCCTCGGTCGCGAATAGGCTTGGATTAACAGAAATTCCTGCTTCTAATTAATACACTGTTTGTGCB
AATCCCATCAUAAAGCATGGATTGATTATGCAAGGACTACTTCACAGACTTAATCACTAACGAGAG
CATTAATTAATTCANAAATGTATAGAGAAATGTATCCCCATAGGCCCGTTATGTGGTGATCAGGCCACGCTG
CGCCCCACGGCCCCGGAGACACAGCCCCACAGTTTCTAAACTGTACCCCAATGCTTCCCAACACATAAAT
CCTATATTAATCTATGCACAAATATGGATAAACACTGGATTATGATACACAGGACCAATGCTGCCCAAT
CCACATGGAAATTTACAACTATTCACAGCCCAAAAGGCTCCAGACTTTGATGTCAATGGATGATTCTGTGG
AGAGGCTGATATACATGCTCGTGGAGACGGGGAGCTGGAGAACTACTACATCAATTTACACCGCGACCAAT
GGTACCAATTTGGCAGTTTGGACTGGTCAAGGGAAATCCATGCCATGACTTTGATATTCGTGTGCC
TTTTTTATTCGCGGTCAGGTATGAAGACAGGATCAATAGTCCCAAGATCGTCTCAACATGACTGCTGG
CCCCACGATCTCTGATATGCTGGGCTCGACACACTCTCTGATGTGGACGGCAAGCTGTCTCCCAAGCT
CTUGACCCAGAAAGACCGAGGTAACAGGTTTCGACAAACAGAGGCCCAAAATTTGGGCTGATACATCTCT
AGTGGAUAGAGCAAAATTTCTAGCTAAGAGAGAAATCCAGCAAAATTCACAACTCAAACTCAAACTGCG
CCAAATATGAACGGGTCAAGAACTATGCCAGAGGCCAGGTACACAGACGCTGTGAACACACCGGGGAG
AATGGGCAATCTGATGAGGATACATCTGGCAAGCTTCGAATTCACAAAGTAAAGAGACCCGATGACCTGCT
CACATCCCGAGAGCAGCGCGGAACCTCTACGCTCGCGCTTCATGACAAAGACAAAGAGTGCAGTGTGA
GGAGTCTGTTTACGCTGCAGCAGAGGCCAAAGAAAGTCAAGGCAATTTTGAAGAAACAGGGGACT
CCAAAGTAAAGCCAGATTTGTCATACCTCGGCAGACAGCTCTCTGTCCGTCGAATTTGAAGGTGAAT
ATATGACATAAATCTGGAAGAAAGAGAAATTCAGTGTGCAACCAAGAAACATTTGCTAAGGCTCATG
ATGAAGGCCCAAGGGGCCAAGAGATCTCCAGGCTCCAGTGTGGCAACAGGGGCCAGGATGCTGGCAGAT
AGCAATACCGCTGGGCCCACTACCACTGTCCGAGTGACACACAAGTGTTTTATTCTCCCAATGACTC
TATCCATTTGAGAGAACTGTACCAATCGGCCAGAGCGCTGGAAGGACCAATAAGGCATACATGACAAAG
AGATTGAAGCTCTCAAAATTAAGAAATTAAGAAATTAAGAAAGTGAAGGACACTGAAGAGAAAGGAGGCT
GAGGAATGAGCTCAGTAAACAAAGCTTATTAATAAGAGAAAGGTGTAAGAAAGCAAGAGAAATTAAG
GAGCCATCTTCAACCAATCAAGGAGGCTGCTCAGGAAGTATGACAACTGCAACTTTTCAAGGAACACA
ACCGTAGAGGAGAAAGGAGAGGAG
CTCACTCTCTTCAAGCATGACAACTACCTGCGACAGACGCCCCGTTCTGGAACCTGGGATCTTTCTGTG
TTGCAAGATCTTCAACAACTACCTACTGTTGTTGCGTACATTAATGAGACGCAATATTTCTTTCTCT
GTGAGTTTGTGACTGGCTTTTGGAGTATTTGATATGAATACAGATCTTATCAGCTTCAAAATTCAGTG
TACACGATGAACAGGAGCTTTGAAATCAGCTACACGTAACTAATGGAGCTCAGAGCTGTCAAGGATA
CAGCTGCAACCAAGACCTTAAGAAATTTGATGTTGGAUATTAAGTGGAGGAAGCTATGACTACACA
CGAGGACAGTTATGGATGATGGGAAGGTAAATCAGCCCGCTCTCACTCGAGACATCAATGGCAAGGCT
AGAGGAGCTACAGTGTGAATGAACATCTATGATGACAGCAAACTACAGACTAGTCTGTTGGTCT
GATCAATTAATTAATGAAGGATTTAGATAGAGATTTGCACTGCTGAAAGTCACTATGAGCAAAATTAACACA
AATAAGACTCAAACTGCTCAAGGTGACGGGTTCTGGTGTGCTCTGCTGAGCAGCTGTGTCATGAGAGAT
GGGCTCTGTGACTCAGTGAAGACCCAGGCATATGGTTGGGAACACCTCATTTGACCTGGCAGCTG
ACCTTCAAAAGCTGATTTGAACGCCAACATTAAGTCAAGAGTGAAGTGAATGAATGAATGAATGAATGAAT
CCAGAGTTAATCAATTAATTTGATCTGACACTGGAGAAACCGAAATTAAGAGGGGCTGAGAGACTTAA
TCTATCGGAUAGCTTTTCAAGTGGGATGATGACATGACAGACTAGAGCTCGGGCCACGCCCGCTGCGAC
CCATTTCCGAGGACCCGGAAGAACTTCCCCAGTATGGTGTCTCGAAAGGACATTTTGAAGATCACTA
TATCTCTGCTGAGATTCGAGTGAATTTCACTTCACTAGATTCACCATGCCCCGCAACCAAGGAG
TAATTCAGACATAGCGGGGAAGATGTTGACCAAGGTGAGAGAAATCAGGAAGGAGAGTACAGACACC
TGAAGGACAGGCTGCTCTTCACTCTCTCTCTGATAGATGAACCTGTACCTACCTTAACCACTGAT
TCTTTTAACTTTTATTTTAACTTAATTAAGGTAACTACAGCCCAACACTTCCAAGCTTCCCTGGGT
ACCTTCTGCACTGAAGCTAGTGAGCATGTGAGCAAGCGGTGCAACGAGACTCACTGATTAATTT
ACTATCTGCAAGAGTAGAAGAAAGGCTGGGATATTTGGGTGGCTGGTTGATTTTGGTGTGT
GTTTGTGTTGATTAACAGTATATCTTTTGAATATCGTAGGACATAAGATATACATGTATCAAT

FIGURE 45A

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CAAGATGGCTAGAATGGTGCCTTTCTGAGTGCTAAACTTGACACCCCTGGTAANCTTTTCACACACTT
CCACTGGCTGGTAATGAAGTTTGTATCATTTTACCACCTGGAAATTTTCAATGCCGTCAATTTTCAGTT
AGATGAIATTGCACTTTTGAGATTAAATGCCAIGTCTATTTGATTAGTCTTATTTTTTATTTTACAGSC
TAAACAGTCCTCACTGTGGCTGTCTTGTGACAAAGTCAATAAACCCCCAGGACGACACAGATGGA
TCACATATTGTTGACATTAAGC11TTGCCAGAAATGTTGCATGTGTTTTACCTCGACITGCTAAATCG
ATTAGCAGAAAGGCATGGCTAATAATGTTGGTGGTGAAATAAATAAATAGTAACAAANRRAARAWGCC
CTGCTCTCTCTGTGGCTAGCCTCAAGCGTTTCATCATACATACCTTTAAGATTGCTATATTTTGGGTT
A1TTCCTTGCACAGGAGAAAAGATCTAAGATCTTTTATTTTCATCTTTTTTGGTTTTCTTGGCATGACTA
AGAAAGCTTAAATG1TGATAAATATGACTAGTTTGAATTTACACCAAGAACTTCTCAATAAAGAAAAAC
ATGAATGCTCCACATTTCAACATAGCACAGAGAGTAA1TCTTAACATGTTTCTTAIGATATTG
TAAGACCTTCCACCAAGTTCTGATACTTTAAAGACATAGTTCAAAATTTGCTTTTGAATCTGTATCTT
GAAATATCTCTGTGTGTATAGG1TTAAATACCAGCTAAAGGATTACCTCACTGAGTCATCAGTACC
CTCCTATTGAGTCCCCAAGATGATGTTTTGCTTACCTTAAGAGAGGTTTTCTCTTAATTTTAGATA
ATTCAAGTGTCTAGATAAATTAAGTTTTCTTTAAGTGTTATGGTAAACTTTTAAAGAAATTTAATAT
GTTATAGCTGAATCTTTTTTGGTAACTTTAAATCTTTATCATAGACTGTGACATATGTTCAATTAAGCTGC
TTGCTGTATGTGTATCATCGGTGGGATGACAGAACAAACATATTTATGATCATGAATATTTGCTTTGT
AANAGATTTCAGTTATTAGGAAGUATACCTGTTTTTATCATGTATAATATTCATGATCTTTAT
AGAACATCTGGCTTCAGGAAGCTAGAGCAATTTCTTCAATAAAAGGTGTTAAATCTTAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 45B

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CAGGAATTCGGCAGGAGGCGGTGCTCCAGAAAGTGGTGGTACTGTCAAGTAGTTAATTCAGCTGGCAGGT
TCCCTGAGTGCAGCTGGCTCGNTAGTCGTAAATGAAGAGTGTGTCCGAAAGACTTTGAATCCAGTATGAA
TGTAGTACAGGAATTAATTTAAAGTCTAGGATCAGAGGGACTGAAGACTGGGCTCCCTCTGATTTCAAA
TCATATTTAAATTCATCCACCACTCAGAGGAGGACCTGTGGTGCAGCCAGAAATTTTTCTGTGCGGGC
TGTGGAACCTCAGTAGAGGCTTAAGTTGTGAGGCGGTCCGGTACTGCGAATACCTAGGGAAGTATTTCTG
TAGCTGCTGCCACTCATATGCGAGGTGCTCATCCTGCCGAATCCTGNTGATGTGGGACITCAAGAAAT
ACTAGGTCAGCAATTTCTCCAAACAGCTGCTCGAGACATATGCCACCAGCCCATTTTCAATTTCTGAGC
ATCGGCGAAAGCCTGTATCGGAAAGCCAGGAGCTGGACAGAGTGAAGGAATTCAGGAGCAGCTCTTCCA
TATCAAGAGAGCTGTTGAAGACCTGTAGGTTTGTATCAGTGCTATTAAGGAGTGTGAGCAGGTGCCGGGA
GACTTGATGATGACTCCAGCTGTCTCCCTTAGGACCTGGTCAAGATCAAGAAAGGGCTGTGGCACCTT
TACTCAAGGACATTCTGAAAGCTTCCCTTGACATGTGCTGGCTGTGAGCTGTGTCAAGGAAGGGCTTT
ATTTGTGAATTTTCCAGAAATCAGCTGTCTATCTTCCCATTCAGACAGCAACATGTAGAAATGTTCAAG
GTTCAGGGCTTGTCTTCAAAACAGCTGCTTCCAGCTCCTCCGAGTCCGCCGGTGTGCGAGGATCAACGGA
GAGAGAACTTCTGGAAAGTGTGGGCTCTCCAGCAACATGATGCCCTGAGTACTGTGAAAAAGACTGTTG
AACATGCCCTTATGATTAACCCGATTTG1GTCTATTATTGGTGAATTGTTTAGATATTGGGATTTGATTA
TTAAGGAAAAAGATGGTCTATATTCTCTTTATTGCAATACCTTAATGTTTCAAAAGAAATCAGATTTCTGTG
TTTAAGCAGAGGGCTGATAGTTGTGGTTTGTTTACAAATGTTCTGTGTTTGGCTGCTATTGGTTTAAAA
GAGGTTTTTATACTTTTGTATTGATAGTTATGTGTTTCACTGATGCTGAGCCAGTTGTTGATGTGTGTGCA
TATATGTGAAGCTGAAGTGAAGATGAATTAAGCTTCTGCTTCAAGCTTGTGATGAAAGCTG
GTTGGTCTTTCAAGTGAHMAAAATATGACCCCAAAAAAAAAAAAAAAAAAAGCAATGCGAAGGTG
CAATATCTGAGCTGTGTGGTGGTGGTCTCGGCTTCTGCTCTGAGCAGCAATGGGCGCAAAAGGAAGAA
CAGGGCCCTCGCCCCACGTTGCTGGACGCCGAACCCGG

FIGURE 46

GGAAATTAAGATCTTCATATTGAATCCATCAGTGATTCAAGAGATACACCTATTGCTTAAACACCTTA
CATGTATTGGTTATGGAATCATGTGTTGGTAGGTTCTTAAGACCTGTTTCTCAAACTCTGACACGTT
TCAAGGAGGGCTTATTGACTTGCACGGTTGGGCAGATTAATCAGATTTACCTAAGATTGGGTAAAAAGT
CTCTGTGACCTTTGCTGGCAGGGCATTGTCTAGTGGAGTACAGGATCTAAAGGGTTTCTTAGAAGGG
CAATATTGTCCAATGAGTAGCAGAGGACTCTGGGTTAGAAGCATCTGCACAAAAACTGSGAGACCTA
CTCTCCACGCTCTGACAGTGGATGGCTGATGSCAGGCTGAGCAGTGGGGAAGCAGGTTTAAACACAGGG
AGTCTTTCAGGTCACCTGTATATTAGNAGAAACATAAACTATTGTCTGTTACATTTCCAGGTCAAGCTTA
CTCTTTACGTTTTATAATATGCAATGCGAGCTTCTGGAAAGCAGTATCATCATGTATCAAAATGCTTTA
TACACCATCAATCATGAATTTTATGACATGGTCAAGACTGTGTGAATATGTCTCTTATGATGATTTGG
GGAGATGTGATTTATTTTCATATTTTCAAAATGCATTTCAATTAAGGTTATCTATTGAGACAAAC
GAAAAAAAAAAAAAAAAA

FIGURE 47

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AATTTTGGSCCCTCCGAAAGGCCAAGAAATTCGGGCCACCGANGGAATTTTGGTACCACCCAGGGGG
 (GSAATGGGAATAGCTGCTTTCAAACCTTAGTTTCCCTTCCATTTCCTTAGTCTGGCCTTTGACACAAAT
 CTGGTAGAAGAGAGCCTGATAAATTTGAGGGCATTGTACCCCTCCCTGTGCCCCAGCAAGGCTTCTGGAGG
 AAGCTCAAGAAATTTGTGAACACGGCGGTGGAGGGGGGGTGAATGGCCATGGCGTGGGCGTCCGATTCAGGC
 CTGGTCAACCTTGGTGGGAGCTTTATCTGTGATCTCATTTGAAATGTTCCAGAGGGAGCATCATAGAAGCCCA
 GAGCTCCGATTTCCAAAGAGCTGATATTGACATTTATGGAGATTGGGTTTGAACATATTTTGAATAACT
 AACCTATTTTGTGGGGTTTGGTTGTCTCTGTCTTAGGACCTGGTAGTTATTTGCTTGATTTTTTTTC
 CGTTATTTCTGCAIAGGCCAAAGAGAATTCGAGGGATAGACAGTCTCCAGAAAAGTAGAGTGGTGGGAGA
 GAATTGCTTTTCTCTTTTCTCTTTCTCTAGTTTCTTTCTGGCTGAGATTTCCGTGCAAGACAGCAG
 CCAATAGACATATAGAGTTGACATTGACATTTAATGGGCGCATGGCTCATTTTGTAGATTGAGAAGG
 TGCTCTCCCTCTGCTCCAGCTCTCATATGACAGCTGTCTGACAGCTGGGAGTCTGTGGCTTCTCTACGG
 AGAGCCCTTAAGCTGGACACTGAAGCAGCCCTAGGCTGGGCAAGGATGGGACCCATGCCCCCTCTTGA
 GAGCGGCTTCTGGTTAGGAAGGACAGCTGGGGGTGCTTGCATAATAGTTCACTGGTCACCTGCTCT
 TATGAGTAGTGTTTTGTGCACTTGGCAGGGTTTCTCTGTGTGCGAGGGGAGTGAATTAAGCAATGG
 TGCTCGGAGTAAGCCTTACAATTTAATAGACTTCTCTATCATATCCCTCATTTCTTCCCTGAATAA
 AATACACACAAAGCAAAAAAATATGATATTTTACATCTCTTAGTTCCTTGCCTGCCCCAACAAGATATCT
 TAGTTCACACTGGCCAGGATTTTCTCTACNAGTCAGAAATACACATTACTAGAGGACACAGCCACCAAGG
 TATTGTGTCTACTTTTATCTGTGCAAGCCACAAATACCCACTTGGMAAGACCATTTGTGATGGGTAA
 ACATCCCTTCTGTCTCCCAACACCCCTGTGACTGGCTTGCATGTGTTCATGACCTCCGMAAGCCCTTAAT
 CAAGAAGCAACAAACCCAGAGATCTCCACCCCTCTCTCAGGACCTCTCTGAAGAGGGGATGAAGTG
 GGTCTCCAGGGAGGCAAGTGGGGGCTTGTGGCAGCTGGGTGGGAGCGGCTTACAGAGGGGAGCTGTG
 CAETTTGGAGGGGCAACCGTCCGAGGAGACAGGCTCTACACACCCCACTCTACTTATCATCTGCTGCT
 CACAAACCCCTTGTCCAGGCTTTATGCACTGGATTTATTTTCCAAATCGAGAGGACATGATGATGCAAT
 TTTGCCCAAGGCTGCTCTCAGAAAGTGCCTAAATGTATATTGTTCAAATCGAGAGGACATGATGATGCAAT
 TTTGGTTTGTGAGCAGTAAAACTCTTCCACTGTGACTTAATTTCTCTCTCAGGAGGCGAGCAGCTGG
 TCCCTTTGTGCTGACTCTAGCAGTGGCCAGGATCCAATACGNGTCCAGGGGTGACCCAGGAGTGGTGGG
 GCGAGCGGCTTCTCCACTACCCAGGCGACCAAGGCCCTGACGCACTGGCTCTGCACTCTAGCAGATCC
 CTGTGCAACGCTGGAGGGTGCATGGCCGCTACCTTTGTTCAGATGGTGGMAAGCTGATGATACAG
 CTCCTTCCCTGCGTGGCCCTGCCACGAGAGCAGGCATTGTGAACCTGCTGGTGTTCGACCTCCCAAGTGGCA
 TGCCCTCCAGCCCMACCCACAGTGGAGACTGGAGACAGGGCAATGAGTCTGGTCCGGGGCAGCTGGACATG
 CCCCATAGGGGCCCCACCCAGACTTAACAGGCAAGGTCTCTGGGACTTGCOCGACGCAAGGACTCAATGCTAA
 ACCAAGGCTGCTGGCTGTGTGCCAGGSCCCTCTCTGATTTACACATCCCATTTTACACAGACCCCTT
 CTCTTTTAAAGGCTGACAGTCTGTTGGCAGCCAGAACCCACACCATGAAGACAGGAGTGAAGGGCC
 TTTGTGCCCAATCCAGCACACCTGCGTCTGSGGTGTGTGAGAGGCATGTTGCTGTCTGTGCGCTGGTGG
 TCTCTGTGAGTCAAGTCCGAGGACGGGAAATTCAGGGGTGTGSGGGCGTGGGCTTATATGTGGAGACTGA
 TGCAGAGTTCCGCTTGCAAGCGATCTGGATATACACTATGTATTAATTTGATGTTAAATATATC
 TGTTTGCCATCTCATGAGAAGATATATGTAAAGGCTCTGAAGGGAGAGGGAGATGTACATTTCTGCCACGGC
 FCTTAGGGACTTATCCGAGTCAATGAATTTGATGACTGTGATCCAGTGGTCAAGAGCTACACTCATG
 TGTGATCAGGCTTATGACTCTAATGTATTTTAAAGGCAAAATGTACGCGGACTCTCATCTACCCCTC
 GATTCCTCTGAGTCCAGGCTTTCTGTGCCAGTGCTTCACTGAGCCACACGCTCTCGCATCCGGGACCGGG
 TGGGCTGAGGCTCTGGGGCACAGTTGCCATGGAGCCCTCTGGGTCTTCTACAAATGTGCTGAGTGGCCA
 UCTGAAGAACCCACAGGAGATGGAGTACCTTGGCCAAAGCTTAAAGAGAAGATTTCTCAGGGTATTTATTA
 GTGTGTCCACAGGCTCAGGAAGCAGGATGGAAAGATCCATTCAGACTGTAATTTATTAACAGAGCAAA
 GATTTTGTGTTCTTATGATGACAGTATTAAGTTTGGGACTTATTTCCATTTGAGAGCTATATATGCT
 ATTTAAGATGATAATTTCTGCTTAAGTTGTGCTTTCAGCTTCAATGAGTTTAAAGAGCATATAGGCTA
 ATGATACCAATGAGGGTTGGTTTATTAACAACCTGAATGACTGTGGTTTCTCCAGTAATTTATTTCTT
 ACTGAACATGGAGCATTTATTAAGAGTGTGTGTTTATATGATGACATTTGATATTTTGTGCTGTG
 TGATGTTCTATTTTCAATAGTTTCTCTTTAGTTTAAAGTTGTGATACGATTTAGATCTGTGCTG
 TAAGTGCATAACAGTGGCTCTGCTGGGTCTCTCTGCTTTTATTTTACTTTAAGGACAGGTGATGTTG
 TCGTCCACACCTCTCAAAAAAGTGAACCTGCCCTGCCCTTTTGTGTCAGACAGCTGTGATACTTGA
 ACCACTTCTACCATACTTATGTGTGTAATCAACCTCTTTTGTGTACATTTATCTCATGCTTCTGCAAA
 TCCGATTAATTTCTATGGCTTCCNN

FIGURE 48

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